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protein search, using sw model ı OM protein

Run on:

March 22, 2006, 15:27:29; Search time 21.0526 Seconds (without alignments) 1828.118 Million cell updates/sec

US-10-797-248A-3 2086

score:

1 MAARNCTKALRPLARQLATP.....IRNLEIWRAGKRSLRPENQK Perfect sc Sequence:

Scoring table:

Gapop 10.0 , Gapext 0.5

of hits satisfying chosen parameters: Total number

283416 seqs, 96216763 residues

Searched:

seq seq

length: 0 length: 2000000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_80:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ketol-acid reducto ketol-acid reducto ketol-acid reducto ketol-acid reducto acetohydroxy acid ketol-acid reducto ketol-acid reducto Description ketol-acid ketol-acid ketol-acid ketol-acid ketol-acid AB1323 T06825 S30145 T45681 C90204 A96911 C84032 D72362 AD2095 A24709 T40532 F70407 AC1694 C69644 JC1428 Length Query Score 484.5 483.480.5 469.5 465 463 463 459.5 458.5 No. Result

ketol-acid reducto	ketol-acid reducto ketol-acid reducto	acetolactate synth ketol-acid reducto	hypothetical prote	ketol-acid reducto	ketol-acid reducto						
G81411 E83059	C48648 E82634	T35830 JC5166	H87120	T45415	G87511	AB3330	B64561	AE2824	D97602	A71945	ISECKR
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405 393	387	378 360	349.	349	335	329.5	329	329	329	325	321
30	3 2	3.4 3.5	36	, ac	3.6	40	41	42	43	44	45

ALIGNMENTS

ketol-acid reductoisomerase (EC 1.1.1.86) - Neurospora crassa N;Alternate names: alpha-keto-beta-hydroxylacyl reductoisomerase

C;Species: Neurospora crassa C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004

C.Accession: JC1428
R.Sista.—H.-Boxman, B.

Gene 120 115-118 1992
A;Title: Characterization of the ilv-2 gene from Neurospora crassa encoding alpha-keto-be
A;Reference number: JC1428; MUID:93013010; PMID:1398116 A;Accession: JC1428
A;Accession: JC1428
A;Molecule type: DNA
A;Residues: 1-400 <51S>
A;Cross-references: UNIPROT:P38674; UNIPARC:UPI000012D525; GB:M84189; NID:g168821; PIDN:;A;Genetics:
A;Genetics:

A;Map position: V A;Introns: 68/1; 78/3; 170/3; 392/3 C;Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase home C;Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrion; oxidoreductase F;87-273/Domain: ketol-acid reductoisomerase homology <KAR>

ö Gaps ö Length 400; Indela Query Match

100.0%; Score 2086; DB 1;
Best Local Similarity 100.0%; Pred. No. 6.9e-146;
Matches 400; Conservative 0; Mismatches 0; ò

9 1 MAARNCTKALRPLARQLATPAVQRRTFVAAASAVRASVAVKAVAAPARQQVRGVKTMDFA 1 MAARNCTKALRPLARQLATPAVQRRTFVAAASAVRASVAVKAVAAPARQQVRGVKTMDFA

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reducto reducto reducto

reducto reducto

ketol-acid ketol-acid alpha-ketoketol-acid ketol-acid

ketol-acid

reducto -beta-hy

ketol-acid

F64492 A47037. F89997

336 331 348 348 334 595

reducto reducto

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S17180 G95051 C97922 C75387 C81801 F81066 B86778

442.5 4332.5 432.5 427.5 427.5 415.5 409

ketol-acid ketol-acid

reducto

120 120 61 GHKEEVHERADWPAEKLLDYFKNDTLALIGYGSQGHGQGLNLRDNGLNVIVGVRKNGKSW 61 GHKEEVHERADWPAEKLLDYFKNDTLALIGYGSQGHGQGLNLRDNGLNVIVGVRKNGKSW ò

180 180 121 EDAIQDGWVPGKNLFDVDEAISRGTIVMNLLSDAAQSETWPHIKPQITKGKTLYFSHGFS ò 요

240 181 PVFKDLTKVEVPTDVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEKAVAL PVFKDLTKVEVPTDVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEKAVAL 181 ઠે В

GVAVGSGYLYETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVE 241 ò

300 300 360

301 EATQSLYPLIGAHGMDWMFDACSTTARRGAIDWTPKFKDALKPVFNNLYDSVKNGDERKR 360 301 EATQSLYPLIGAHGMDWMFDACSTTARRGAIDWTPKFKDALKPVFNNLYDSVKNGDERKR g g ð

361 SLEYNSQPDYRERYEAELDEIRNLEIWRAGKRSLRPENQK 400

8

ketol-acid reducto probable ketol-aci ketol-acid reducto

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A;Experimental source: strain PR745 C;Genetics:
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Matches 287; Conservative
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A;Map position: 2
C;Function:
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Ketol-acid reductoisomerase (EC 1.1.1.86) ILV5 - yeast (Saccharomyces cerevisiae)

Ketol-acid reductoisomerase (EC 1.1.1.86) ILV5 - yeast (Saccharomyces cerevisiae)

Ketol-acid reductoisomerase (EC 1.1.1.86) ILV5 - yeast (Saccharomyces cerevisiae)

C; Materiae Saccharomyces cerevisiae

C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004

C; Accession: A4709; S31463

R; Petersen, JG.L.; Holmberg, S.

Nucleic Acids Res. 14, 9631-9651, 1986

A; Title: The ILV5 gene of Saccharomyces cerevisiae is highly expressed.

A; Title: The ILV5 gene of Saccharomyces cerevisiae is highly expressed.

A; Reference number: A24709; MUID: 87117524; PMID: 3027658

A; Molecule type: DNA

A; Mesidues: 1-395 < PET>
A; Residues: 1-395 < PET>
A; Residues: 1-395 < PET>
A; CVS SACCHAROMS 
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C,Species: Schizosaccharomyces pombe
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, December 1994
A; Description: The sequence of S. cerevisiae cosmid 9638.
A; Reference number: S51459
A; Reference number: S51453
A; Molecule type: DNA
A; Residues: 1-395 < DUZ>
A; Cross-references: UNIPARC: UPI000012D529; EMBL: U19102; NID:g609396; PIDN: AAB67753.1; C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Map position: 12R
C;Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase
C;Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrion; oxidoreductase
F;81-267/Domain: ketol-acid reductoisomerase homology <KAR>
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Query Match 72.3%; Score 1508.5; DB 1 Best Local Similarity 73.6%; Pred. No. 2.1e-103; Matches 295; Conservative 39; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: SGD:ILV5; MIPS:YLR355c
A;Cross-references: SGD:S0004347; MIPS:YLR355c
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A;Pathway: branched-chain amino acid biosynthesis
C;Superfamily: Ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase homc
C;Keywords: isoleucine-valine biosynthesis; isomerase; oxidoreductase
F;88-274/Domain: ketol-acid reductoisomerase homology <KAR>
    В. G.
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    M.H.; Rajandream, M.A.; Barrell,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 SVKNGDERKRSLEYNSQPDYRERYEAELDEIRNLEIWRAGK--RSLRPENQK 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AARNCTKALRPL-ARQLATPAVQRRTFVAAASAVRASVAVKAVAAPARQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.6%; Score 1494.5; DB 2; Length 69.7%; Pred. No. 2.4e-102; ive 52; Mismatches 46; Indels
R; Purnelle, B.; Goffeau, A.; Wood, V.; Lyne, submitted to the EMBL Data Library, May 1998
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242

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Gispecies: Listeria innocua
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
RGlaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: ilvC
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ketol-acid reductoisomerase (acetohydroxy-acid isomeroreductase) homolog ilvC [imported]
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A;Cross-references: UNIPARC:UPI0000CC759; GB:AL592022; PIDN:CAC97323.1; PID:g16414607;
A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                 194 DVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEKAVALGVAVG---SGYLY 250
                                                                                                                                                                                                                                                                                                                                                                     243 YERGFTGMLKAVSDTAKYGGLTVGPKVIDDHVKENMKKFAERVRSGEFAK---EWISKAD 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 GAHGMDWMFDACSTTARRGAIDWTPK-FKDALKPVFNNLYDSVKNGDERKRSLEYNSQPD 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKLLDYFKNDTLALIGYGSQGHGQGLNLRDNGLNVIVGVRKNGKSWEDAIQDGWVPGKNL 134
                                                                                                                                                                                    FDVDEAISRGTIVMNLLSDAAQSETW-PHIKPQITKGKTLYFSHGFSPVFKDLTKVEVPT 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 YEGGMEKMRHSISNTAEYG--DYVSGPRVVTADTKKAMKEVLTDIONGNFAKSFIDDNKN 296
                                                                                    ETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEATQSLYPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||||: | ||| ||: |:||: |:||: |: || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 KASEVLEELMKPIEEHEIEKVGR 322
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Best Local
Matches 1
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                      C; Species: Aquifex accilius
C; Species: Aquifex accilius
C; Species: Aquifex accilius
C; Accession: P70407
R; Deckert, G; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.B.; Ov. V.
C; Accession: P70407
N; Dature 392, 353-358, 1998
A; Title: The complete genome of the hyperthermophilic bacterium Aquifex acolicus.
A; Reference number: A70300; MUID: 98196666; PMID: 9537320
A; Reference number: A70300; MUID: 98196666; PMID: 9537320
A; Residues: P70407
A; Residues: P70407
A; Residues: UNIPROT: O67289; UNIPARC: UPI0000056582; GB: AE000730; NID: 92983674; PI
A; Experimental source: strain VF5
C; Generics:
A; Gene: iv.C
C; Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase homology < KAR>
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C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisc
F;24-206/Domain: ketol-acid reductoisomerase homology «KAR»
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A;Cross-references: UNIPROT:09UZ09; UNIPARC:UPI000003453B; GB:AJ248287; GB:AL096836; NID
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
C;Accession: H75049
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome
A;Reference number: A75001
A;Accession: H75044
A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ketol-acid reductoisomerase (ilvc) PAB0889 - Pyrococcus abyssi (strain Orsay)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.8%; Score 497; DB 2; Length 33 Best Local Similarity 34.7%; Pred. No. 4.6e-29; Matches 115; Conservative 70; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.3%; Score 486; DB 2; Length 33: 37.8%; Pred. No. 3e-28; ive 63; Mismatches 120; Indels
acetohydroxy acid isomeroreductase - Aquifex aeolicus
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Best Local Simi
Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12
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C;Genetics:

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C;Accession: AB1323

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat A;Title. Comparative genomics of Listeria species.
A;Reference number: AB1077; MUD:21537279; PMID:11679669
A;Accession. AB1323
A;Accession. AB1323
A;Molecule type: DNA
A;Residues: 1-331 <GLA>
A;Cross-references: UNIPARC:UPI0000054FF8; GB:NC_003210; PIDN:CAD00064.1; PID:gl6411439; CGGenetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 480.5; DB 2;
; Pred. No. 7.5e-28;
52; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.0%;
37.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.0%
Best Local Similarity 37.9%
Matches 124; Conservative
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C66644

ketol-acid reductoisomerase ilvC - Bacillus subtilis
C15pecies: Bacillus Signates
C2 Brown, Signates
C3 Brown, Signates
C3 Brown, Signates
C4 Brown, Signates
C5 Brown, Signates
C6 Brown, Signates
C6 Brown, Signates
C7 Brown, Signates
C8 Brown, Signates
C
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A;Cross-references: UNIPROT:P37253; UNIPARC:UP10000038DEE; GB:Z99118; GB:AL009126; NID:g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: ilvC
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisc
F;21-202/Domain: ketol-acid reductoisomerase homology <KAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 GKNLFDVDEAISRGTIVMNLLSDAAQSETW-PHIKPQITKGKTLYFSHGFSPVFKDLTKV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 EVPTDVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEKAVALGVAVG---S 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 GYLYETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEATQSL 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 YPLIGAHGMDWMFDACSTTARRGAIDWTPKFKDA-LKPVFNNLYDSVKNGDERKRSLEYN 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
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Pred. No. 5.2e-28;
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23.2%; Score 483; DB 2; Length 34
Best Local Similarity 38.3%; Pred. No. 5.2e-28;
Matches 119; Conservative 58; Mismatches 108; Indels
                                                                                              GFKEFHRMRKEQOGHQIEKVGAELREM 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 SQPDYRERYEA 376
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Indels

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A,Gene: pgaair
C,Superfamily: ketol-acid reductoisomerase, plant type; ketol-acid reductoisomerase homol
C,Keywords: isoleucine-valine biosynthesis; isomerase; oxidoreductase
F;113-311/Domain: ketol-acid reductoisomerase homology <KAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: Z15837
A;Accession: T06825
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T06825
A;Accule type: mRNA
A;Residues: 1-581 <ZHU>
A;Accoss-references: UNIPROT:082043; UNIPARC:UPI000012D526; EMBL:Y17796; PIDN:CAA76854.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                         ETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEATQSLYPLI 310
                                                                                                                                       134 LFDVDEAISRGTIVMNLLSDAAQSETWPH-IKPQITKGKTLYFSHGFSPVFKDLTKVEVP 192
                                                                                                                                                                                                                                                                    TDVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEKAV--ALGVAVGSGYLY 250
                                                                                                                                                                                                                                                                                                                                                                                                                                               311 GAHGMDWMFDACSTTARRGAIDW-----TPKFKDALKPVFNNL-----YDSVKN 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 YEGGMEKMRHSISNTÄEYG--DYVSGPRVVTADTKKAMKEVLTDIONGNFAKSFINDNKN 296
                                                                     62
                                                                                                                                                                      63 VYSVSEAADKADVIMILLPDETQGETYENEIKPNLKAGNSLVFAHGFNIHF---DVINPP
                                                                                                                                                                                                                                                                                                           ketol_acid reductoisomerase (EC 1.1.1.86) - garden pea
C;Species: Pisum sativum (garden pea)
C;Species: 23.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 05-Oct-2004
C;Accession: T06825
R;Zhu, X.
submitted to the EMBL Data Library, August 1998
79 DYFKND----TLALIGYGSQGHGQGLNLRDNGLNVIVGVRKNGKSWEDAIQDGWVPGKN
                                      DAVKNNALEGKTVAVIGYGSQGHAHSQNLKDNGNNVIIGIRE-GKSAESARNDGF----D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDERKRSLEYNSQPDYRERYEAELDEI 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : | | |: | | 323
GFKEFHRMRKEQOGHOIEKVGAELREM 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 26.8
Matches 140; Conservative
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ketol-acid reductoisomerase (acetohydroxy-acid isomeroreductase) homolog ilvC [imported]

C;Species: Listeria monocyrogenes

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
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65

Gaps

232

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VHERADWPAEKLLDYFKN-DTLALIGYGSQGHGQGLNLRD-----NGLNVIVGVRKNGK 118
                                                                                                                                                                                                                                                                                  341 LAYKNTVECITGTISRTISTQGMLAVYNSLSEEGKKDFETAYSASFYPCMEILYECYEDV 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 QSGSEIRSVVLAGRRFYEKEGLPAFPMGNIDQTRMWKVGERVRKSRPAGDLGPLYPFTAG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----MFLAQYEVLRERGHSPSEAFNETVEEATQSLYPLIGAHGMDWMFDACSTTARRGAI 331
                                                                                                                                                                      7 TKALRPLARQLATPAVQRRTFVAAASAVRASVAVKA-VAAPARQQVRGVKTMDFAGHKEE
                                                                                                                                                                                                                                                                                                                                             SWEDAIQDGWV-PGKNLFDVDEAISRGTIVMNLLSDAAQSETWPHIKPQITKGKTLYFSH
                                                                                                                                                                                                                                                                                                                                                                                                                                GFSPVFKDLTKVEVPTDVDV1LVAPKGSGRTVRSLFREGR-----GINSSFAVYODVTGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 TKALRPLARQLATPAVQRRTFVAAASAVRASVAVKA-VAAPARQQVRGVKTMDFAGHKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 AKEKAVALGVAVGSGYLYETTFEKEVYSDLYGERGCLMGGIHG------
    F;1-67/Domain: transit peptide (chloroplast) #status predicted <TNP>F;68-591/Product: ketol-acid reductoisomerase #status predicted <MAT>F;123-321/Domain: ketol-acid reductoisomerase homology <KAR>
                                                                                     Query Match 22.3%; Score 465; DB 1; Length 591;
Best Local Similarity 27.2%; Pred. No. 2.3e-26;
Matches 132; Conservative 68; Mismatches 128; Indels 158;
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                                                                                                                                                                                                                                                                                                                                             119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ketol-acid reductoisomerase (EC 1.1.1.86) precursor - Arabidopsis thaliana N;Alternate names: acetohydroxy acid isomeroreductase C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 05-Oct-2004 C;Accession: S30145; S34040; S36884 R;Curien, G.; Dumas, R.; Douce, R. R;Curien, G.; Dumas, R.; Douce, R. Biol. 21, 717-722, 1993 A;Title: Nucleotide sequence and characterization of a cDNA encoding the acetohydroxy ac A;Reference number: S30145; MUID:93192533; PMID:8448371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Genome: nuclear
A;Genome: nuclear
A;Introns: 99/3; 130/3; 152/3; 199/3; 275/3; 315/1; 361/3; 417/3; 469/3
C;Superfamily: ketol-acid reductoisomerase, plant type; ketol-acid reductoisomerase home
C;Keywords: chloroplast; isoleucine-valine biosynthesis; isomerase; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-284, 'R', 286-591 <DUM>
A; Residues: 1-284, 'R', 286-591 <DUM>
A; Cross-references: UNIPARC:UPI000016DB7B; EMBL:X68150; NID:9288062; PIDN:CAA48253.1; PI
A; Curien, G.; DeRose, R.T.; Douce, R.
Biochem. J. 294, 821-828, 1993
A; Title: Branched-chain-amino-acid biosynthesis in plants: molecular cloning and charact
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A;Residues: 1-578,'A',580-591 <DU2>
A;Cross-references: UNIPARC:UP10000000A7B; EMBL:X69880; NID:g402551; PIDN:CAA49506.1;
                                                                                                               LIGYGSQCHGQCLNLRD-----NGLNVIVGVRKNGKSWEDAIQDGWVPGK-NLFDVDEA 140
                                                                                                                                                                                          141 ISRGTIVMNLLSDAAQSETWPHIKPQITKGKTLYFSHGFSPVFKDLTKVEVPTDVDVILV 200
                                                                                                                                                                                                                                                                           201 APKGSGRTVRSLFREGR----GINSSFAVYQDVTGKAKEKAVALGVAVGSGYLYETTFE 255
                                                                                                                                                                                                                                                                                                                                                            234 CPKGMGPSVRRLYVQGKEINGAGINSSFGVHQDVDGRATNVALGMSVALGSPFTFATTLE 293
                                                                                                                                                                                                                                                                                                                                                                                                                              275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :|| || || || || 414 AFPMGKIDQTRMWKVGERVRSTRPAGDLGPLYPFTAGVFVAMMAQIEVLRKKGHSYSEI 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --- MFLAQYEVLRERGHSPSEA 294
      40
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                          -AVORRTFVAAASAVRASVAV
                                                                                 KAVAAPARQQVRGVKTMDF------AGHKEEVHERADWPAEKLLDYFKN-DTLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: S36884; MUID:93393563; PMID:8379936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Dumas, R. submitted to the EMBL Data Library, July 1992 A; Reference number: 834040
                                                                                                                                                                                                                                                                                                                                                                                                                        KEVYSDLYGERGCLMGGIHG------
MAA - - RNCTKALRPLAROLATP
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A; Residues: 1-591 < CUR>
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A,Map position: 3
A;Introns: 99/3, 130/3; 152/3; 199/3; 275/3; 315/1; 361/3; 417/3; 469/3
A;Note: F14P22.200
C;Superfamily: ketol-acid reductoisomerase, plant type; ketol-acid reductoisomerase homol
F;123-321/Domain: ketol-acid reductoisomerase homology <KAR>
ketol-acid reductoisomerase - Arabidopsis thaliana
NyAlternate names: protein F14P22.200
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 05-Oct-2004
C;Accession: T44681
R;D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.
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Best Local Similarity 27.2%; Pred. No. 2.3e-26;
Matches 132; Conservative 68; Mismatches 128; Indels 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-591 cDAN>
A;Cross-references: UNIPROT:Q05758; UNIPARC:UPI0000000A7B;
A;Experimental source: cultivar Columbia; BAC clone F14P22 C;Genetics:
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us-10-797-248a-3.rpr

GMFLAQYEVLRERGHSPSI	Query Match Query Matches 135; Indels 20; Gaps 9; Maraches 118; Conservative 62; Maraches 135; Indels 20; Gaps 9; Query Matches Maraches 128; Indels 20; Gaps 9; Query Match Maraches 128; Indels 20; Gaps 9; Query Match Maraches 128; Indels 20; Gaps 9; Query 124 IODGAVPCKULPVDEALGECTURALIGYGGGGANLENDGIAVIGYGKKGARDA 123 Query 124 IODGAVPCKULPVDALGECTURALIGYGGGTARGANLIGYGGARGAN 59 Query 139 FKDLTKVEVPTDVULLNAPKGSGRTVASLFREGGRINSFANGENIN 115 Query 183 FKDLTKVEVPTDVULLNAPKGSGRTVASLFREGGRINSFANGENIN 115 Query 183 FKDLTKVEVPTDVULLNAPKGSGRTVASLFREGGRINSFANGENIN 115 Query 183 FKDLTKVEVPTDVULLNAPKGSGRTVASLFREGGRINSFANGENIN 115 Query 184 AVGEVYLVEVPTEKEVSDLTGAGGAGFCLYANHODYGKKKEKAALAGK 172 Query 184 AVGSGTLYETTPEKGASCANLOGGICALINAGYDTKREAGYSRERAPENETUR 300 113 GIGGTKGGVANTTFKIETETDLFGEQAVLCGGICALINAGYDTKREAGYSRENAPECH 232 Query 185 MAGNITVDLARGGGANAGGRING 185
	SULT 12 0204 tol-acid reductoisome Species: Sulfolobus s Accession: C90204 Shocession: C90204 Show Q.; Singh, R.K.; Show Corner, R.A.; Ragan, M. Description: Sulfolobos Reference number: A99 Reference number: A99 Reference number: A99 Residues: 1-335 «KUR- Cross-references: UNI Genetics: Gene: ilvC-1 Genetics: Genetic

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A;Accession: C84032
A;Status: preliminary
A;Alcaule: preliminary
A;Alcaule: preliminary
A;Alcaule: 1-340 «STO»
A;Residues: 1-340 «STO»
A;Cross-references: UNIPROT:Q9K8E7; UNIPARC:UP1000012D53B; GB:AP001517; GB:BA000004; NID
A;Cross-references: strain C-125
C;Genetics:
C;Genetics:
A;Gene: ilvC
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: D72362
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A.Reference number: A72200; MUID:99287316; PMID:10360571
A.Accession: D72362
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A;Cross-references: UNIPROT:09WZ20; UNIPARC:UPI000012D560; GB:AE001730; GB:AE000512; NIC
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: TM0550
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisc
F;21-203/Domain: ketol-acid reductoisomerase homology <KAR>
                                                                                                                                                                                                                                                                                                                                    85 TLALIGYGSQGHGQGLNLRDNGLNVIVGVRKNGKSWEDAIQDGWVPGKNLFDVDEAISRG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSGRTVRSLFREGRGINSSFAVYQDVTGKAKEKAVALGVAVGSGY--LYETTFEKEVYSD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 LFGEQAVLCGGTSALVKAGFETLVEAGYQPEVAYFECLHE-LKLIVDLMYEGGLEYMRYS 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 DEAISRGTIVMNLLSDAAQSETW-PHIKPQITKGKTLYFSHGFSPVFKDLTKVEVPTDVD 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 TIVMNLLSDAAQSETWPH-IKPQITKGKTLYFSHGFSPVFKDLTKVEVPTDVDVILVAPK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 LYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEATQSLYPLIGAHGMDWMFDA 321
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                                                                                                                                                                                                                                                                                                                                                               C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #Bequence_revision 11-Jun-1999 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                      22.0%; Score 458.5; DB 2; Length 336; 37.9%; Pred. No. 3.2e-26; tive 57; Mismatches 104; Indels 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 CSTTARRGAIDWTPKF----KDALKPVFNNL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 22.09
Best Local Similarity 39.39
Matches 107; Conservative
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Best Local Similarity 37.9
Matches 106; Conservative
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Search completed: March 22, 2006, 15:34:34 Job time: 22.0526 secs

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OM protein protein search, using sw model

Run on: March 22, 2006, 15:27:29 ; Search time 20.7895 Seconds (without alignments 1828.118 Million ce cell updates/sec

Perfect score: Title: US-10-797-248A-2 2071

Sequence:

MLRTQAARLICNSRVITAKR......RNMEIWKVGKEVRKLRPENQ 395

Gapop 10.0 , Gapext 0.5

Scoring table:

BLOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

Maximum 80 80 eq Beq length: 0 length: 2000000000

Minimum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pu and is derived by analysis of the total score distribution. printed

SUMMARIES

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366	340	595	332	336.	340	331	333	581	337	337	591	591	363	334	367	340	342	331	336	335	331	337	348	333	332	404	400	395	,
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E82634	B86778	S17180	H69497	G95051	C97922	AD2095	A69059	T06825	F81066	C81801	T45681	S30145	C75387	F89997	A47037	C84032	C69644	AB1323	D72362	C90204	AC1694~	A96911	F64492	F70407	H75044	T40532	JC1428	A24709	ID
ketol-acid reducto	-acid			l-acid	ketol-acid reducto	-acid		1-acid	1-acid	-acid	l-acid		acid	-keto-	-acid	-acid	-acid	-acid	-acid				ketol-acid reducto	×			ketol-acid reducto	l-acid redu	! !

	43			_	-						33		31 3	30
335	336	336	339	339	339	50.5	50.5	52.5	357	59.5	365	369	72.5	385
16.2	16.2	16.2	16.4	16.4	16.4	16.9	16.9	17.0	17.2	17.4	17.6	17.8	18.0	18.6
492	333	333	491	491	491	339	339	339	333	338	338	332	344	340
NN	N	N	N	N	_	N	N	2	۳	۲	N	N	۲	N
T45415 AG0473	H87120	D70855	E86063	D91217	ISECKR	D97602	AE2824	AB3330	JC5166	C48648	臣83059	T35830	S35140	G81411
keto1-acid reducto	ketol-acid reducto	probable ilvC prot	ketol-acid reducto	ketol-acid reducto	ketol-acid reducto	hypothetical prote	ketol-acid reducto	acetolactate synth	probable ketol-aci	ketol-acid reducto				

ALIGNMENTS

ketol-acid reductoisomerase (EC 1.1.1.86) ILV5 - yeast (Saccharomyces cerevisiae) N;Alternate names: acetohydroxyacid reductoisomerase ILV5; protein L9638.7; protein YLR3: C;Species: Saccharomyces cerevisiae

Species: Saccharomyces cerevisiae Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004

C;Accession: A24709; S51463

R;Petersen, J.G.L.; Holmberg, S.

NOCIEIC Acids Res: 14, 9631-9651, 1986

A;Title: The IDV5 gene or Saccharomyces cerevisiae is highly expressed.

A;Reference number: A24709; MUID:87117524; PMID:3027658

A;Accession: A24709;

A; Molecule type: DNA A; Residues: 1-395 < PET>

Cross-references: UNIPROT: P06168; UNIPARC: UPI000012D529; EMBL: X04969; NID: g3826; PIDN: (

submitted to the EMBL Data Library, December 1994 A;Description: The sequence of S. cerevisiae cosmid 9638 A;Reference number: S51459

A; Accession: S51463

A;Molecule type: DNA A;Residues: 1-395 <DUZ> A;Cross-references: UNIPARC:UPI000012D529; EMBL:U19102; NID:g609396; PIDN:AAB67753.1; Genetics:

PII

A; Gene: SGD:ILV5; MIPS:YLR355c

A;Cross-references: SGD:S0004347; MIPS:YLR355c
A;Map position: 12R
G;Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid re C;Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrion; F;81-267/Domain: ketol-acid reductoisomerase homology <KAR> reductoisomerase home oxidoreductase

Ś 밁 밁 S 밁 Ś 밁 5 Matches Query Match Best Local Similarity 181 121 181 121 GWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGKTLYFSHGFSPVFKDL 395; 61 61 -THVEPPKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVAIGS YERADWPREKLLDYFKNDTFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWKAAIED 120 GWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGKTLYFSHGFSPVFKDL YERADWPREKLLDYFKNDTFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWKAAIED MLRTQAARLICNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETV MLRTQAARLICNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETV THVEPPKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVAIGS 100.0%; Score 2071; DB 1; ilarity 100.0%; Pred. No. 1.4e-147; Conservative 0; Mismatches 0; DB 1; Length 395; Indels 0, Gaps 180 240 180 120 60 0

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241 GYVYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEATQSL 300

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Retol-acid reductoisomerase (EC 1.1.1.86) - Neurospora crassa
N/Alternate names: alpha-keto-beta-hydroxylacyl reductoisomerase
C/Species: Neurospora crassa
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C/Accession: JC1428
R/Sista, H.; Bowman, B.
Gene 120, 115-118, 1992
A,7Title: Characterization of the ilv-2 gene from Neurospora crassa encoding alpha-keto-b
A,Reference number: JC1428; MUID:93013010; PMID:1398116
A,Accession: JC1428
A,Molecule type: DNA
A,Cross-references: UNIPROT:P38674; UNIPARC:UPI000012D525; GB:M84189; NID:g168821; PIDN:
C/Genetics:
A,Gene: ilv-2
A,Map position: V
A,Introns: 68/1; 78/3; 170/3; 392/3
A,Introns: 68/1; 78/3; 170/3; 392/3
A,Introns: 68/1; 78/3; 170/3; 392/3
C/Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase hom
C/Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrion; oxidoreductase
F,87-273/Domain: ketol-acid reductoisomerase homology <KAR>
ketol-acid reductoisomerase (EC 1.1.1.86)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-
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                                                                                                                                 SLEYNSQPDYRERYEAELDEIRNLEIWRAGK--RSLRPENQ
                                                                                                                                                                  SLEFNSOPDYREKLEKELDTIRNMEIWKVGKEVRKLRPENO 395
                                                                                                                                                                                                                                            EATQSLYPLIGKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKR
                                                                                                                                                                                                                                                                                                      AVAIGSGYVYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTVETVYERADWPREKLLDYFKNDTFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASW
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73.6%; Pred. No. 2.16
tive 39; Mismatches
   03-Dec-1999
                                      [similarity] - fission yeast
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2.1e-105;
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   05-Oct-2004
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                                        (Schizosaccharom)
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RESULT H75044

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A; Rescription: S.pombe ILVS homolog.
A; Reference number: Z22407
A; Accession: T43303
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Fesidues: Z62-404 < KAN>
A; Cross-references: UNIPARC:UPI0000168765; EMBL:AB009603; NID:g2696653; PIDN:BAA24000.1;
R; Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
NA Res. 4, 363-369, 1997
A; Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A; Reference number: Z17323; MUID:98162722; PMID:9501991
A; Reference number: Z17323; MUID:98162722; PMID:9501991
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-37, R', 39-40, W', 42-91, S', 93-237, T', 239-274, P', 276-296, P', 298-393, G', EMBL:DBS-274, P', 27
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R;Purnelle, B.; Goffeau, A.; Wood, V.; Lyne, submitted to the EMBL Data Library, May 1998
A;Reference number: Z21935
A;Accession: T40532
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A; Residues: 1-404 < PUR>
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                                                     PDYREKLEKELDTIRNMEIWKVGKEVRKLRPEN
                                                                                                                                                            PLIGKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFNSQ
                                                                                                                                                                                                                                FIYQTTFKKEVISDLVGERGCLMGGINGLFLAQYQVLRERGHSPAEAFNETVEEATQSLY
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                                                                                                                PLIGKYGLDYMFAACSTTARRGAIDWTPRFLEANKKVLNELYDNVENGNEAKRSLEYNSA
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70.2%;
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A; Molecule type: DNA
A; Residues: 1-333 <AQF>
A; Cross-references: UNIPROT:067289;
A; Cross-references: Btrain VF5
                                                           A;Gene: ilvC
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type;
F;21-203/Domain: ketol-acid reductoisomerase homology <KAR>
                                                                                                                                                                                               A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: F70407
                                                                                                                                                                                                                                                            C;Accession: ...
R;Deckert, G.; Warren,
                                                                                                                                                                                                                                                                                            acetohydroxy acid isomeroreductase - Aquifex aeolicus c;Species: Aquifex aeolicus c;Species: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Oct-2004 C;Accession: F70407
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C;Superfamily: ketol-acid reductoisomerase, a
F;24-206/Domain: ketol-acid reductoisomerase
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submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus
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A; Accession: H75044
                                                                                                                                                                                  A;Status: preliminary; nucleic acid
                                                                                                                                                                                                                                                 Nature 392,
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                                                                                                            Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTIEEAVKRADIVHILIPDLVQPKVYREHIEPYLREGQALGFSHGFNIHYKQIV---PPE
23.4%;
nilarity 35.6%;
Conservative 6
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                                                                                                                                                                                                                                                                            P.V.; Gaasterland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.9%; Score 495; DB 2; 38.2%; Pred. No. 1.5e-29;
   64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60;
Score 485.5; DB 2
Pred. No. 7.7e-29;
4; Mismatches 129
                                                                                                                                    UNIPARC: UPI0000056582; GB: AE000730; NID: g2983674;
                                                                                                                                                                                 sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence:
                                                                                                                                                                                                                                                                          T.; Young, W.G.; Lenox,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 archaea/bacteria type;
                                                                                                                                                                                                                                                                                                                                                                                                                     327
                                                                                                                                                                                    not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology
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                              DB 2;
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                            Length
 Indels
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 17;
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                                                                                                                                                                                                                                                                            A.L.; Graham,
                                                                           ketol-acid
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                                                                                                    ISGMRYSISDTAKYGDVTRGERIYKVVKPVMEKTLEEIQKGEFAREWILENKAGRPVYYA 303
                                                                                                                                                                                                                                                                                                                                                                VILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVAIGS--GYVYQTTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDILKDKVIAILGYGSQGHAHALNLRDSGLNVIIGLHEGSRSREKAKADGF----EVYTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDYFKNDTFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWKAAIEDGWVPGKNLFTV 131
                                                KLEKELDTIRNMEIWKVGKEVRKLRP 392
                                                                                                                                                       MDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFN--SQPDYRE
                                                                                                                                                                                                           KEETETDLFGEQMVLCGGVTALIKAGFETLVNAGYQPEVAYFECLHE-LKLIVDLIYEHG
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                                                                                                                                                                                                                                                                                                                                                                                                                    REAAKRADIIMFLIPDTVQPEVYKNEVEPELNSSKTLAFAHGFNIHFRQIV---PPKDVD
LLERD----REHLVEKVGEELRKMMP 325
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Ribult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glod rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; W.A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jan A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: F64492
                                                                                                     A;Map position: FOR1521365-1522411
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ket C;Kupvords: isoleucine-valine biosynthesis; isomerase; oxidoreductase F;39-221/Domain: ketol-acid reductoisomerase homology <KAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ketol-acid reductoisomerase (EC 1.1.1.86) - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: 10-Sep_1999 #sequence_revision 10-Sep_1999 #text_change 05-Oct-2004 C;Accession: F64492
                                                                                                                                                                                                                                                 A;Cross-references: UNIPARC:UPI0000165FEC; GB:U67595; GB:L77117; C;Genetics:
                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-348 < BUL>
                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not
                                      Query Match
          Local
      Similarity
23.1%;
      Score 478; DB 1
Pred. No. 3e-28;
                                  DB 1;
                                  Length 348
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Methanococcus jannaschii
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                                                                                                                                                                           ketol-acid
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197

VIQTTFREETETDLFGEQVVLCGGVTELIKAAFETLVEAGYAPEMAYFETCHE-LKLIVD VYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEATQSLYP 302 PPENVNITMVAPKSPGAMVRKTYEEGFGVPGLVAVERDYTGDALQIALGMAKGIGLTKVG PPKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVAIG--SGY 242 HKVMTIEEAAEKADIIHILIPDEVQPAVYKKQIEPYLTEGKTISFSHGYNIHY---GFIR 136

255

243

256 303

LIYQKGLQGMWENVSNTAEYGGLTRRARVINEESRKAMKEILKEIQDGRFAKEWSLE---

LIGKYGMDYMYDACSTTARRGALDWYP-IFKNALKPVFQDLYESTKNGTETKR-SLEFNS

137

126 KNLFTVEDAIKRGSYVMNLLSDAAQSETW-PAIKPLLTKGKTLYFSHGFSPVFKDLTHVE 184

66 WPREKLLDYFKNDTFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWKAAIEDGWVPG 125

YDKDVTFDAVKDKTTAVIGYGSQGRAQALNMKDSGLNVIVGLRPNGASWNKAIKD----G 79

118;

Conservative

67;

Mismatches 125;

Indels

Gaps

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AC1694
ketol-acid reductoisomerase (acetohydroxy-acid isomeroreductase)
C;Species: Listeria innocua
C;Species: C7-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 0
C;Accession: AC1694
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.;
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.;
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1694
A;Statue: preliminary
A;Molecule type: DNA
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R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q97MV0; UNIPARC:UPI00000C9D5C; GB:AE001437; PIDN:AAK78076.1 A;Experimental source: Clostridium acetobutylicum ATCC824 C;Genetics: A;Gene: CAC0091 C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase.
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A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325
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A; Residues: 1-337 < KUR>
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; Entian, K.
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Voss, H.; W
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Fsihi, H.
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Wehland,
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A;Molecule type: DNA A;Residues: 1-335 <KUR> A;Residues: 1-335 <KUR> A;Residues: 1-335 <KUR> A;Cross-references: UNIPROT:Q9UWX9; UNIPARC:UPI000012D50D; GB:AE006641; NID:g13813740; C;Genetics: 1vC-1 A;Gene: ilvC-1 A;Gene: ilvC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Reddarrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-331 <GLA>
A;Cross-references: UNIPARC:UPI00000CC759; GB:AL592022; PIDN:CAC97323.1; PID:g16414607; (A;Experimental source: strain Clip11262
A;Experics:
C;Genetics:
A;Gene: ilvC
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Sulfolobi
C;Date: 24-May-2001
C;Accession: C90204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: C90204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A99139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ketol-acid reductoisomerase (ilvC-1) [imported] - Sulfolobus solfataricus
                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change
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Best Local
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                                                                                                                                                                                                                                                                                                                     Local Similarity
  128
                                                                                                                                                 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 DYFKND----TFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWKAAIEDGWVPGKN
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                                                                                                                                                                                             LDLIKGKRIAVLGYGSQGRAWAQNLRDSGLNVVVGLEREGKSWELAKSDGITP----LHT
                                                                                                                                                                                                                                              LDYFKNDTFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWKAAIEDGWVPGKNLFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKYGMDYMYDACSTTARRGALDWYPIF-----KNALKPVFQDLYESTKNGTETKRSLEFN
VYMIAPKGPGPTVREYYKAGGGVPALVAVHQDVSGTALHKALAIAKGIGATRAGVIPTTF
                                           VILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVAIGS--GYVYQTTF
                                                                                                 KDAVKDADIIIFLVPDMVQRTLWLESVQPYMKKGADLVFAHGFNIHYK---LIDPPKDSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVAIGS--GYVY
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                                                                                                                                                                                                                                                                                            22.6%; Score 468; DB 2; I 34.4%; Pred. No. 1.6e-27; tive 65; Mismatches 129;
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                                                                                                                                                                                                                                                                                                                                          Length 335;
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A;Gene: TM0550
C;Superfamily:
F;21-203/Domain
ketol-acid reductoisomerase (acetohydroxy-acid isomeroreductase) homolog il-
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
C;Accession: AB1223
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.!
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AB1323
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R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ketol-acid reductoisomerase - 7
C;Species: Thermotoga maritima
C;Date: 11-Un-199 #sequence_1
C;Accession: D72362
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A; Residues: 1-336 < ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A72200;
A;Accession: D72362
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A; Title: Evidence for
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Best Local S
Matches 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; 21-203/Domain: ketol-acid reductoisomerase homology <KAR>
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mes 117; Conserv
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                                                                                                                                                                                                        FYTMRKKESEHL----IEKVGKELRKMMP
                                                                                                                                                                                                                                                                                        LSFMRYSVSNTAEYG--DYISQEKIVTKEVRENMKQMLKDIQTGKFAKDWILENQAGRPY
                                                                                                                                                                                                                                                                                                                         MDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEF----NSQPD
                                                                                                                                                                                                                                                                                                                                                                   KEETETDLFGEQAVLCGGVTALIKAGFETLVDAGYQPEIAYFECLNE-LKLIVDLIYEGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lateral gene transfer between Archaea 2200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.6%; Score 468; DB 2; 35.6%; Pred. No. 1.6e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - Thermotoga maritima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 124;
                                                                                                                                                                                                        326
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  Berche, P.
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    Bloecker
Fsihi, H.
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on, D.;
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Science 294, 849-852, 2001

A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AB1323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-331 <GLA>
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Best Local
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                                                                                                                                                                                                                                                                                                                       245
                                                                                                                                                                                                                                                                                                                                                                                                                                                         187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 LFTVEDAIKRGSYYMILLSDAAQSETWP-AIKPLLTKGKTLYFSHGFSPVFKDLTHVEPP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 VYSVSEAADKADVIMILLPDETQGETYENEIKPNLKAGNSLVFAHGFNIHF-DV--INPP 119
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                                                                                                                                                                                              GKYGMDYMYDACSTTARRGALDWYPIF----KNALKPVFQDLYESTKNGTETKRSLEFN 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAVKNNALEGKTVAVIGYGSQGHAHSQNLRDNGNNVIIGIR-EGKSAESARNDGF----D 62
KN-GFKEFHRMRKEQ---QGHQIEKVGAELREMMP 325
                                                        SOPDYRE--KLEKELDTIRNMEIWKVGKEVRKLRP 392
                                                                                                                               YEGGMEKMRHSISNTAEYGDYVSGPRVVTADTKKAMKEVLTDI----
                                                                                                                                                                                                                                                                                                                   QTTFEREVNSDLYGERGCIMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEATQSLYPLI 304
                                                                                                                                                                                                                                                                                                                                                                                         SDVDVFLVAPKGPGHLVRRTFVEGGAVPSLFAIYQDATGNARDTALSYAKGIGATRAGVI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVAIGS--GYVY 244
                                                                                                                                                                                                                                                       ETTFKEETETDLFGEQAVLCGGATHLIQAGFETLVEAGYQPELAYFEVLHE-MKLIVDLM
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Pred. No. 2.6e-27;
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RESULT 12
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C69644

ketol-acid reductoisomerase ilvC - C;Species: Bacillus subtilis Bacillus subtilis

C;Date: 05-De C;Accession: Species: Bacillus subtilis; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004;

C69644

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterr C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chon, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B. Mature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadaie, Y.; Sato, T.M.; Portetelle, R.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, A.; Winters: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, A.; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A.; Status: preliminary; nucleic acid sequence not shown; translation not shown A.; Experimental source: strain 168

A;Cross-references: UNIPROT:p37253; UNIPARC:UPI0000038DEE; GB:Z99118; GB:AL009126; NID:g2.

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C;Accession: C84032
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C84032
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A;Gene: ilvC
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoiso
C;Superfamily: ketol-acid reductoisomerase homology <KAR>
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004
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C84032
ketol-acid reductoisomerase ilvC [imported] - Bacillus halodurans (strain C-125)
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Best Local S
Matches 112
                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics:
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Best Local
  191
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                                                                                                                                                                                                                                                                                                                                                  h 21.4%; Score 443.5; DB 2; Length 340;
Similarity 35.0%; Pred. No. 1.1e-25;
12; Conservative 61; Mismatches 128; Indels 19
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                                      LYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEATQSLYPLIGKYGMDYMYDA
                                                                                    GPGHLVRRTYVDGAGVPGLVAVYQDATGQAKDIALAYSKMNGSARAGVIETTFQEETETD
                                                                                                                                                                        DVIMILLPDEHQPTVYKNBIBPELSEGKTLAFAHGFNVHFNQIV---PPATVDVFLAAPK
                                                                                                                                                                                                                   SYVMNLLSDAAQSETWP-AIKPLLTKGKTLYFSHGFSPVFKDLTHVEPPKDLDVILVAPK 197
                                                                                                                                                                                                                                                EFN--SOPDYREKLEKELDTIRNMEIWKVGKEVRKLRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLIGKYGMDYMYDACSTTARRGALDWYP-----IFKNALKPVFQDLYESTKNGTETKRSL 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKNLFTVEDAIKRGSYVMNLLSDAAQSETWPA-IKPLLTKGKTLYFSHGFSPVFKDLTHV 183
LFGEQAVLCGGTSALVKAGFETLVEAGYQPEVAYFECLHE-LKLIVDLMYEGGLEYMRYS
                                                                                                                          GSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVAIGSGY--VYQTTFEREVNSD
                                                                                                                                                                                                                                                                                                         TFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWKAAIEDGWVPGKNLFTVEDAIKRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -VYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEATQSLY 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHKVFSVKEAAAQAEIIMVLLPDEQQQKVYEAEIKDELTAGKSLVFAHGFNVHFHQIV--
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A;Molecule type: DNA; protein
A;Residues: 37-327,'A',329-367 <RIE>
A;Cross-references: UNIPARC:UPI0000171F81
A;Experimental source: PCC 6803
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J. Bacteriol. 174, 7910-7918, 1992
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C;Accession: S76754; A47037
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UPI0000164C81; EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:EA;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S76754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ketol-acid reductoisomerase (EC 1.1.1.86) C;Species: Synechocystis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoison;Keywords: isoleucine-valine biosynthesis; isomerase; oxidoreductase
;Keywords: isoleucine-valine biosynthesis; isomerase; oxidoreductase
;57-239/Domain: ketol-acid reductoisomerase homology <KAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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     300
                                                         329
                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                             211 RGINSSYAVWNDVTGKAHEKAQALAVAIGS--GYVYQTTFEREVNSDLYGERGCLMGGIH
                                                                                                                                                                                                                                                                                                                                    124 TVYEAETAPHLVAGNVLLFAHGFNINF---AQIVPPADVDVVMAAPKGPGHLVRRTYEQG
                                                                                                                                                                                                                                                                                                                                                                                       152 ETWPA-IKPLLTKGKTLYFSHGFSPVFKDLTHVEPPKDLDVILVAPKGSGRTVRSLFKEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al Similarity
116; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 HALNLKDSGVNVVVGLYSGSKS--VAKAEG--AGLKVLSVAEAAKAADLIMILLPDEVQK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 QGLNLRDNGLNVIIGVRKDGASWKAAIEDGWVPGKNLFTVEDAIKRGSYVMNLLSDAAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14
                                                      P-IFKNALKPVFQDLYESTKNGTETKRSLEFN--SQPDYREKLEKELDTIRNMEIWKVGK 385
                                                                                                               ALIKAGFDTLVEAGYQPELAYFECLHE-VKLIVDLIVEGGLAKMRDSISNTAEYGDLTRG
                                                                                                                                                                   GMFLAQYDVLRENGHSPSEAFNETVEEATQSLYPLIGKYGMDYMYDACSTTARRGALDWY 328
                                                                                                                                                                                                                         QGVPALFAVYQDASGQARDYAMAYAKGIGGTRAGILETTFREETETDLFGEQVVLCGGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRPAFAMIKSLQSTIQSQQ-----GDSYMARMYYDQDANLDLLAGKTVAIIGYGSQGHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRPAARFVKPMITTRGLKQINFGGTVETVYERADWPREKLLDYFKNDTFALIGYGSQGYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.3%; Score 442; DB 1; ilarity 31.8%; Pred. No. 1.6e-25; Conservative 72; Mismatches 153

    Synechocystis sp.

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e homology <KAR>
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C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Accession: F89997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha-keto-beta-hydroxylacil reductoisomerase [imported] - Staphylococcus aureus (strain
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 05-Oct-2004
C;Accession: F89997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-334 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 21.3%; Score 441.5; DB 2; Length 334; Best Local Similarity 34.1%; Pred. No. 1.5e-25; Matches 118; Conservative 68; Mismatches 125; Indels 35;
                                                                                                                                                                                                               171
                                                      349
                                                                                                                                                                                                                                          238 IGS--GYVYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEE 295
                                                                                                                                                                                                                                                                                                                                                             178 KDLTHVEPPKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVA 237
                                                                                                                                                                                                                                                                                                              114 ---GVIQPPADVDVFLVAPKGPGHLVRRTFVEGSAVPSLFGIQQDASGQARNIALSYAKG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 EDGWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWP-AIKPLLTKGKTLYFSHGFSPVF 177
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284 GNFSNRFIEDNKN-GFKEFYKLREEQ---HGHQIEKVGRELREMMP 325
                                                                                                  231 -MKLIVDLMYEGGMENVRYSISNTAEFG--DYVSGPRVITPDVKENMKAVLTDI----QN
                                                                                                                                                      296 ATQSLYPLIGKYGMDYMYDACSTTARRGALDWY-----PIFKNALKPVFQDLYESTKN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58
                                                 GTETKRSLEFNSQPDYRE--KLEKELDTIRNMEIWKVGKEVRKLRP 392
                                                                                                                                                                                                       IGATRAGVIETTFKEETETDLFGEQAVLCGGVSKLIQSGFETLVEAGYQPELAYFEVLHE
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Search completed: March 22, 2006, 15:34:33 Job time : 21.7895 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein

Run on:

March 22, 2006, 15:21:02 ; Search time 115.529 Seconds
 (without alignments)
1528.885 Million cell updates/sec

US-10-797-248A-1

Perfect score: Sequence:

Scoring table:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 2443163 seqs, 439378781 residues Searched:

2443163

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003as:* geneseqp2003as:* geneseqp2003as:* geneseqp1980s:* geneseqp2005s:* A_Geneseq_21:* 1: genesecm198 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Abr64303 Acetobydr			Abr64305 Acetohydr	Adv16810 M gramini	7 AE			Abj25877 Aspergill		Abp73238 Candida a	Abr64304 Acetohydr	Adk64188 Disease t			Aau01250 B. subtil	Abb48168 Listeria	Abu32456 Protein e	Aab96356 Putative	Abu24174 Protein e	Abu18526 Protein e	m	Aay26180 Corn acet	l Plant
SUMMARIES	ΩI	ABR64303	ABR64306	ADV16807	ABR64305 .	ADV16810	ABJ26477	ABJ26502	ABJ25902	ABJ25877	AAU15089	ABP73238	ABR64304	ADK64188	ADB70124	ABU20976	AAU01250	ABB48168	ABU32456	AAB96356	ABU24174	ABU18526	AAY26183	AAY26180	ADX93651
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di	Query Match	100.0	99.4	99.4	98.6	79.8	79.7	79.7	78.0	78.0	72.9	72.9	71.8	71.8	6.79	52.6	23.4	22.7	22.7	22.6	22.5	22.4	22.3	22.3	22.3
	Score	2094	2081	2081	1856	1671	1668	1668	1634	1634	1526.5	1526.5	1503	1503	1421.5	1100.5	490	475	475	473	472	469.5	468	468	468
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Adx88429 Plant ful Ady07198 Plant ful Ady07344 Plant ful	Adx77584 Plant ful Aag35210 Zea mays Aag35209 Zea mays	0 0 4		Adr94886 Novel S. Aea58756 Streptoco Ady61069 Abiotic s	Hypert Plant Plant	Plant Plant Soybea S. epi
ADX88429 ADY07198 ADY07344	ADX77584 AAG35210 AAG35209	AAU37780 AAU38003 ABU00804	ABU45897 ADK47367	ADR94886 AEA58756 ADY61069	ADM26226 ADY04361 ADY07450	ADX92449 ADY07435 AAY26182 AAG81458
888	8 M M	440	989	დ თ თ	r & &	,
5886	590 579 596	340 340 340	340	351 351 581	326 571 568	578 626 586 334
22.3 22.3	22.3 22.3	22.1 22.1 22.1	22.1	22.1 22.1 22.1	22.0 21.9 21.8	21.8 21.8 21.6 21.6
468 468 468	468 467 467	462.5 462.5 462.5	462.5	462.5 462.5 462	461.5 458 457	457 457 452 451.5
25 26 27	3 7 8 3 7 8	31 33 33	3.5	334	39 4 4 1 0	4 4 4 4 2 6 4 7

ALIGNMENTS

Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase. Acetohydroxyacid isomeroreductase #1. ABR64303 standard; protein; 402 AA. 16-SEP-2003 (first entry) Magnaporthe grisea. ABR64303; ABR64303 ID ABR6 RESULT 1

FR2829363-A1. 14-MAR-2003.

(AVET) AVENTIS CROPSCIENCE SA. 10-SEP-2001; 2001FR-00011689.

10-SEP-2001; 2001FR-00011689.

Zundel JL, Lebrun MH, Dumas R,

Morin

Effantin G,

Treatment of crops, useful for controlling fungi on, e.g. cereals, potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid isomeroreductase. WPI; 2003-405775/39.

Claim 2; Fig 1; 66pp; French.

The present invention relates to a method for controlling fungal disease in crops by applying an inhibitor (I) of acetohydroxyacid isomeroreductase. (I) are used for curative or preventative treatment of a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or rape. The present sequence is an acetohydroxyacid isomeroreductase, used to illustrate the invention

Sequence 402 AA;

ö Gaps ô Indels Query Match
100.0%; Score 2094; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.4e-191;
Matches 402; Conservative 0; Mismatches 0;

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61 KEQVWERADWPKEKLLEYFKDDTLALIGYGSQGHQQGINLRDNGLNVIIGVRKDGKSWKD 120
                                                                                                                                                                                         121 AVQDGWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHGFSPV 180
                                                                                                                                                                                                                                                                                                                                               301 TQSLYPLIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQRSL 360
                                                                                                                                                                                                                                                                                                                                                                301 TQSLYPLIGANGMDMMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQRSL 360
                                                                        1 MSARGFSKALRPMARQLATPAVQRRTFVAASSMVRATRKAAVAPTQQQIRGVKTMDFAGH
                                                                                                                  KEQVWERADWPKEKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSWKD
                                                                                                                                                                       121 AVQDGWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHGFSPV
                                                                                                                                                                                                                                                181 FKDLTKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIALGV
                                                                                                                                                                                                                                                                                        241 AIGSGYLYKTTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEA
                                                                                                                                                                                                                                                                                                        241 AIGSGYLYKTTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEA
                                                                                                                                                                                                                               181 FKDLTKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIALGV
                                                         1 MSARGFSKALRPMARQLATPAVQRRSFVAASSMVRATRKAAVAPTQQQIRGVKTMDFAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tanzer MM, Hamer L, Adachi K, Dezwaan TM, Lo SC;
Montenegro-Chamorro MV, Darveaux BA, Frank SA, Heiniger
Mahanty SK, Pan H, Covington AS, Tarpey R, Shuster JR;
                                                                                                                                                                                                                                                                                                                                                                                                       361 DYNSOPDYREKYEAEMEEIRNLEIWRAGKAVRSLRPENOK 400
                                                                                                                                                                                                                                                                                                                                                                                                                       361 DYNSQPDYREKYEAEMEEIRNLEIWRAGKAVRSLRPENQK 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    substrate inhibition; antibiotic; gene disruption;
ketol-acid reductoisomerase; ILV5; enzyme.
 Score 2081; DB 6;
Pred. No. 2.5e-190;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAY-2003; 2003US-0470947P.
19-MAY-2003; 2003US-0471615P.
21-MAY-2003; 2003US-0472242P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-2004; 2004WO-US015404.
  99.4%;
99.8%;
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N-PSDB; ADV16805, ADV16806.
Query Match
Best Local Similarity 99.8
Matches 399; Conservative
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                                                                                                                               The present invention relates to a method for controlling fungal disease in crops by applying an inhibitor (I) of acetohydroxyacid isomeroreductase. (I) are used for curative or preventative treatment of a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or rape. The present sequence is an acetohydroxyacid isomeroreductase, used to illustrate the invention
                                                         120
                                                                       AIGSGYLYKTTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEA 300
                                                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                                                  360
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                                                                                                               AVQDGWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHGFSPV 180
                                                                                                                                                                                                                                                                                     TOSLYPLIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQRSL 360
                          9
                                                                                                                                                                                       AIGSGYLYKTTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEA
                                                                                                                                                                                                                                                                                                       antifungal; fungal disease; acetohydroxyacid isomeroreductase.
                KEQVWERADWPKEKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSWKD
MSARGFSKALRPMARQLATPAVQRRSFVAASSMVRATRKAAVAPTQQQIRGVKTMDFAGH
                                                                                                                                                                      PKDLTKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIALGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g. cereals,
of acetohydroxy
                                                                                                                                                                                                                                                                                                                                                            DYNSQPDYREKYEAEMEEIRNLEIWRAGKAVRSLRPENOKOK 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fungi on, e inhibitor o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treatment of crops, useful for controlling potato, cotton or rape, comprises applying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Effantin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 57-58; 66pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acetohydroxyacid isomeroreductas #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zundel JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                               ABR64306 standard; protein; 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AVET ) AVENTIS CROPSCIENCE SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-SEP-2001; 2001FR-00011689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-2001; 2001FR-00011689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ACC80185, ACC80186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lebrun MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-405775/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    potato, cotton or isomeroreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FR2829363-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dumas
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RESULT

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Identifying a test compound as a candidate for an antibiotic comprises contacting ornithine carbamoytransferase (OCTase) or ketol-acid reductoisomerase polypeptide, or fungal pathogenicity-conferring gene
                                                                                                                                                                                                                                                Claim 48; SEQ ID NO 6; 179pp; English.
                                                                                                                                                        with a test compound
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Sequence 400 AA;

RW;

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Morin

Effantin G,

Zundel JL,

Lebrun MH,

Dumas R,

(AVET) AVENTIS CROPSCIENCE SA. 10-SEP-2001; 2001FR-00011689

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candidate for an antibiotic comprising or cure. Compount as a candidate for an antibiotic comprising contacting or cure carbamoytransferase (OCTase) or ketol-acid reductoisomerase polypeptide, or fungal pathoganicity-conferring gane with a test compound. The method comprises: contacting OCTase polypeptide, ketol-acid reductoisomerase polypeptide, or fungal pathoganicity-conferring gene with a test compound or and detecting the presence or absence of binding between the test compound and the polypeptide or absence of binding indicates that the test compound and the polypeptide or an antibiotic. Also described are: an isolated nucleic acid comprising a nucleotide sequence encoding a polypeptide having at least 50% sequence identity to, or having or 10% of the activity of, 400, 403 or 469 amino acids; and an isolated or 469 amino acids. The methods are useful for identifying inhibitors of crithine carbamoytransferase, ketol-acid reductoisomerase, and fungal pathoganicity-conferring gene as antibiotics. This is the amino acid
                                         compound as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence of Magnaporthe grisea ketol-acid reductoisomerase ILV5
                                         identifying
                                      invention describes a method
%$9999999999999998888
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Sequence 400 AA;

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                                                                                                                                  AVQDGWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHGFSPV 180
                                                                                                                                                                                                                         AIGSGYLYKTTPEKEVYSDLYGERGCIMGGIHGMPLAQYEVLRERGHSPSEAFNETVEEA 300
                                                                                                                                                                                                                                                                     TQSLYPLIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQRSL 360
                                                                                                                                                                                                                                                                                   1 MSARGFSKALRPMARQLATPAVQRRTFVAASSMVRATRKAAVAPTQQQIRGVKTMDFAGH 60
                                                                                                                                                                                           FKDLTKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIALGV
                                          1 MSARGFSKALRPMARQLATPAVQRRSFVAASSMVRATRKAAVAPTQQQIRGVKTMDFAGH
                         Gaps
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   Length 400;
                        0; Indels
                                                                                                                                                                                                                                                                                                                DYNSOPDYREKYEAEMEEIRNLEIWRAGKAVRSLRPENOK 400
                                                                                                                                                                                                                                                                                                                              Score 2081; DB 9;
Pred. No. 2.5e-190;
1; Mismatches 0;
 99.4%;
Query Match
Best Local Similarity 99.8
Matches 399; Conservative
                                                                                       61
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Acetohydroxyacid isomeroreductase.
        ABR64305 standard; protein; 400
                          (first entry
                          16-SEP-2003
                 ABR64305;
   RESULT
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Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase

Neurospora crassa FR2829363-A1

Mycosphaerella graminicola

WO2004104176-A2

10-SEP-2001; 2001FR-00011689

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fungi on, e.g. cereals,
inhibitor of acetohydroxy acid
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                                                                                                                                                                                                           The present invention relates to a method for controlling fungal disease in crops by applying an inhibitor (I) of acetohydroxyacid isomeroreductase. (I) are used for curative or preventative treatment of a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or rape. The present sequence is an acetohydroxyacid isomeroreductase, used to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GVAVGSGYLYETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVE 300
                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 PVFKDLTKVEVPTDVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEKAVAL
                                                                                                                                                                                                                                                                                                                                                                                                                1 MSARGFSKALRPMARQLATPAVQRRSFVAASSMVRAT--RKAAVAPTQQQIRGVKTMDFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GHKEQVWERADWPKEKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDAVQDGWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVFKDLTKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVAIGSGYLYKTTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EATQSLYPLIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQR
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                            Length 400;
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359 SLDYNSQPDYREKYEAEMEEIRNLEIWRAGKAVRSLRPENOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          substrate inhibition; antibiotic; gene disruption; ketol-acid reductoisomerase; KAR1; enzyme.
                                                                                                                                                                                                                                                                                                                                         88.6%; Score 1856; DB 6;
86.8%; Pred. No. 9.6e-169;
iive 35; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M graminicola ketol-acid reductoisomerase KAR1
                                                                                                                          Treatment of crops, useful for controlling potato, cotton or rape, comprises applying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADV16810 standard; protein; 403
                                                                                                                                                                                  Claim 2; Fig 1; 66pp; French.
                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 86.8%
Matches 349; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                               WPI; 2003-405775/39
                                                                                                                                                        isomeroreductase.
                                                                                                                                                                                                                                                                                                                Sequence 400 AA;
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                                                                                                                                                                                                                                                                                                                                          Query Match
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ADV16810
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Sequence 396 AA;
                                                                                          4BJ26477
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                                                                                                                              The invention describes a method of identifying a test compound as a candidate for an antibiotic comprising contacting contithine candidate for an antibiotic comprising contacting contithine carbamoytransferase (OcTase) or Ketol-acid reductoisomerase polypeptide, or fungal pathogenicity-conferring gene with a test compound. The method comprises: contacting OcTase polypeptide, ketol-acid reductoisomerase polypeptide, or fungal pathogenicity-conferring gene with a test compound; and detecting the presence or absence of binding between the test compound and the polypeptide or gene, where binding indicates that the cest compound is a candidate for an antibiotic. Also described are: an isolated nucleic acid comprising a nucleotide sequence encoding a polypeptide having at least 50% sequence identity to, or having at least 10% of the activity of, 400, 403 or 469 amino acids and an isolated polypeptide consisting essentially of the amino acid sequence of 400, or 469 amino acids and inibitors of or 469 amino acids carbamoytransferase, ketol-acid reductoisomerase, and fungal pathogenicity-conferring gene as antibiotics. This is the amino acid captoconferring gene as antibiotics. This is the amino acid sequence of Mycosphaerella graminicola ketol-acid reductoisomerase KARI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 FAGHKEQVWERADWPKEKLLEYPKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FAGDXEXVFERDDWPREKTLEYFKNDTLALIGYGSQGHGQGLNLRDNGLNVIVGVRKGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWKDAVQDGWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHG 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                         Identifying a test compound as a candidate for an antibiotic comprises contacting ornithine carbamoytransferase (OCTase) or ketol-acid reductoisomerase polypeptide, or fungal pathogenicity-conferring gene with a test compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALGVAVGSGYMYKTTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERCHSPSEAFNET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSARGFSKALRPMARQLATPAVORRSFVAASSMVRAT----RKAAVAPTQQQIRGVKTMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4,
                                                                                                                                                                            Lo SC;
SA. Heiniger RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 403;
                                                                                                                                                                                                                  Shuster JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.8%; Score 1671; DB 9; 78.4%; Pred. No. 5.4e-151;
                                                                                                                                                                              achi K, Dezwaan TM, Lo
Darveaux BA, Frank SA,
ington AS, Tarpey R, Sl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 50; SEQ ID NO 9; 179pp; English.
                                                                                                                                                                                                                                                                         N-PSDB; ADV16802, ADV16808, ADV16809.
                                                                                                                                                                                                                  Covington AS,
                                                                                                                                                                                Adachi K,
                                                                                                                                          (PARA-) PARADIGM GENETICS INC
                                  17-MAY-2004; 2004WO-US015404.
                                                                      15-MAY-2003; 2003US-0470947P.
                                                                                     19-MAY-2003; 2003US-0471615P.
21-MAY-2003; 2003US-0472242P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 78.4 Matches 315; Conservative
                                                                                                                                                                                                 Montenegro-Chamorro MV,
                                                                                                                                                                                Hamer L,
                                                                                                                                                                                                                  Mahanty SK, Pan H,
                                                                                                                                                                                                                                                      WPI; 2005-021202/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 403 AA;
02-DEC-2004
                                                                                                                                                                                Tanzer MM,
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat a non-infectious by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a chergensing recombinant protein for characterisation, screening or expressing recombinant protein for characterisation, screening or characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologus essential or virulence genes for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identify inhibitors of the binding occurs or to identify inhibitors of the binding cure or to identify inhibitors of the binding certer or response, as a reagent in assays designed to quantitatively determine levels of the protein or organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence for factors. This sequence represents a protein of one of the essential genes or of Aspergillus fumigatus of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lemieux
                                         361 QRITMEYAGRKDYREAFEKEMEEIRNLEIWRAGKAVRSLRPEN 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hu ₩,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus fumigatus essential gene protein #1135.
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                                                                                                                                                                                                                                                                                                    ABJ26477 standard; protein; 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-APR-2001; 2001US-0287066P.
05-JUN-2001; 2001US-029890P.
05-JUN-2001; 2001US-030899P.
31-AUG-2001; 2001US-0316362P.
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357
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DSKETVYERADWPREKLQEYFKNDTLALIGYGSQGHQGGINLRDQGLNVIVGVRKDGASW 114
                                                                                                                                                           KDAVQDGWVPGKNLFEVDRAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHGFS 178
                                                                                                                                                                                                                PVFKDLTKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIAL 238
                                                                                                                                                                                                                                                                    GVAIGSGYLYKTTFEKBVYSDLYGERGCLMGGIHGMPLAQYEVLRERGHSPSEAFNETVE 298
                                                                                                                                                                                                                                                                                                                        EATQSLYPLIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQR 358
                                                                                                                                                                                                                                                                                                                                                   EATOSLYPLICANGMDWMYAACSTTARRGAIDWSSRFKDTLKPIFNELYDSVRDGTETKR 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response.
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                                                                                                                                                                          GVAVGSGYLYETTFEKEVYSDLYGERGCLMGGIHGMPLAQYEVLRERGHSPSEAFNETVE
                                                    MSARGFSKALRPMARQLATPAVQRRSFVAASSMVRATRKAA--VAPTQQQIRGVKTMDFA
                                                                            MASRGLPRALR-LAR-VAAP----RTVISAALPRPALAKAATRVAASTAPVRGVKTIAFA
                                                                                                         GHKEQVWERADWPKEKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSW
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    Length 396;
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1e-150;
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79.7%; Score 1668; D
79.1%; Pred. No. 1e-1
ive 42; Mismatches
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05-JUN-2001; 2001US-0295890P.
09-JUL-2001; 2001US-0303899P.
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contamination;
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the invention are used to treat our prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar blochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune
                                                                                                                                                                                                                                                                                                          response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.7%; Score 1668; DB 6; Length 508; 79.1%; Pred. No. 1.5e-150; ive 42; Mismatches 34; Indels 8
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Best Local Similarity
Matches 318; Conserv
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or expressing recombinant protein for characterisation, screening or expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic crganisms invade or resaide, for comparing with the DNA sequences of A. (uniquatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns. for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit annother immune response, and for identifying polyuncleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for lost issues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This sequence represente a protein of one of the essential genes of Aspergillus fumigatus of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      purified or isolated nucleic acids of
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27-APR-2001; 2001US-0287066P.
05-JUN-2001; 2001US-02990P.
09-JUL-2001; 2001US-031899P.
31-AUG-2001; 2001US-0316362P.
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                        Aspergillus fumigatus.
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Sequence 388 AA;

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55 DSKETVYERADWPREKLOEYFKNDTLALIGYGSQGHQGGLNLRDQGLNVIVGVRKDGASW 114
                                                                                                                                                                                                 119 KDAVQDGWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHGFS 178
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                                                                                   1 MSARGFSKALRPMARQLATPAVQRRSFVAASSMVRATRKAA--VAPTQQQIRGVKTMDFA
                                                                                                                                   59 GHKEQVWERADWPKEKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSW
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     Length 388;
                                    33; Indels
78.0%; Score 1634; DB 6;
78.9%; Pred. No. 1.8e-147;
clive 42; Mismatches 33;
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294 Fungicide, cytostatic, essential gene, Aspergillus fumigatus, infection, cancer, contamination, biofilm, antibody, immune response. EATQSLYPLIGANGWDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQR Lemieux Hu W, Aspergillus fumigatus essential gene protein #535 Eroshkin AM, SLDYNSOPDYREKYEAEMEEIRNLEIWRAGKAVR 392 Ş Zamudio C, ABJ25877 standard; protein; 500 23-APR-2001; 2001US-0285697P. 27-APR-2001; 2001US-0287066F. 05-UUN-2001; 2001US-0295890P. 09-UUL-2001; 2001US-031899F. 31-AUG-2001; 2001US-0316362P. 23-APR-2002; 2002WO-US013142. (first entry) ELIT-) ELITRA PHARM INC Aspergillus fumigatus Tishkoff D, WO200286090-A2 16-APR-2003 239 235 299 359 Jiang B, ABJ25877; ABJ25877 RESULT CCCCCCCCCCCCCCX8X444X8X44488X64X8X8X8X8X8X8X8X8X8X8X ద ò ò d ò g

Lemieux SM

Hu W,

Eroshkin AM,

New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer. WPI; 2003-093124/08.

Disclosure; Page; 175pp; English.

The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infectious by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fumigatus or the polymucleotides are useful for expressing recombinant protein for characterisation, screening or corganisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA captures of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination or expression patterns, for raising anti-DNA antibodies or to elicit another immune corganisms, and for identifying polymucleotides encoding the other protein

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                                                                                                                                                                                                           59 GHKEQVWERADWPKEKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSW 118
                                                                                                                                                                                                                                                              EATQSLYPLIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQR 358
                                                                                                                                                                                                                                                                                                KDAVQDGWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHGFS 178
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                                                                                                                                          78.0%; Score 1634; DB 6; Length 500; 78.9%; Pred. No. 2.7e-147; ive 42; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLDYNSOPDYREKYEAEMEEIRNLEIWRAGKAVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU15089 standard; protein; 400
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                                                                                                                                                                    Matches 311; Conservative
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gene replacement and
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                                                                                                                                                        Local Similarity
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                                                                                                                   Sequence 500 AA;
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                                                                                                                                            Query Match
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strains useful for identification and validation of gene products as targets for therapeutic agents, for creating a collection of identified essential genes, and screening assays for the discovery of new drugs. The invention provides the GRACE (gene replacement and conditional expression) method for the construction of mutant organisms referred to as GRACE strains of the organism. The invention can be applied to any organism, particularly a pathogenic fungus e.g. Candida albicans, Aspezgillus funigatus and Cryptococcus neoformans. The methods are useful to identify agents that may be used in the treatment of fungal infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVFKDLTHVEPPSNIDVILAAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAEEKAIAM 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358
                                                                                                                                                                                                                                                                                                                                                                                                                                             GHKEQVWERADWPKEKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSW 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 GVAIGSGYLYKTTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EATQSLYPLIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQR
               fungal metabolisms and identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fungus, yeast, tetracyclin, promoter, GRACE strain, blosynthesis, signal transduction, DNA replication, cell division, growth, proliferation, Candida albicans, fungicide, antifungal.
                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                  72.9%; Score 1526.5; DB 4; Length 400; 73.8%; Pred. No. 3.9e-137; ive 49; Mismatches 53; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      359 SLDYNSQPDYREKYEAEMEEIRNLEIWRAGKAVRSLRPENQ 399
            ig genes essential to fungal metabolisms and
therapeutic agents that target these genes.
                                                                                       relates to novel methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Candida albicans essential protein SEQ ID NO 7075.
                                                         Claim 43; Page 222-223; 324pp; English.
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Matches 296; Conservative
                                                                                     present invention
                                                                                                                                                                                                                                                                                       Sequence 400 AA;
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                                                                                                                                                                                                                                                            essential genes
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            Identifying
potential th
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Treatment of crops, useful for controlling fungi on, e.g. cereals, potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid isomeroreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method for controlling fungal disease in crops by applying an inhibitor (I) of acetohydroxyacid isomeroreductase. (I) are used for curative or preventative treatment of a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or rape. The present sequence is an acetohydroxyacid isomeroreductase, used
300 BATQSLYPLIGKYGMDYMYDACSTTARRGALDWYPRFKDALKPVFEELYESVKNGSETKR 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIALGVAIGS 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THVEPPKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWDVTGKAHEKAQALAVAIGS
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                                                                                                          360 SLEFNSRSDYKERLEEELQTIRNMEIWRVGKEVRKLRPENQ 400
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                                                                                                                                                                                                                                                                                                                                                                                                                             Acetohydroxyacid isomeroreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zundel JL,
                                                                                                                                                                                                                                                              ABR64304 standard; protein; 395
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Best Local Similarity 72.9%
Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cone allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by insertions or promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene that contributes to the survival or growth of a fungus, a gene that is sesential to the survival or growth of a fungus to an antifungal contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian capant, an antifungal agent that inhibits the growth of a diploid fungus of activity of a gene product, preferably enzymatic activity, carbon compound catabolism, blosyntheric, transporter, transcriptional, compound catabolism, blosyntheric, transporter, transcriptional, compound catabolism, blosyntheric, transporter, transcriptional, compound studied is useful for identifying a compound having the ability to inhibit growth or proliferation of c. albicans cells and cesential candida albicans protein useful in the method of the invention. Note: The sequence data for this parent is not represented in the printed continued by the Ruraman parent of the present is not represented in the printed the Ruraman parent of the present is not represented in the printed continued to the present is not represented in the printed continued to the present is provinted to permether the printed continued to the present is provint
                                                                                                                                                                                                                                                                                                                                                                 Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 44; SEQ ID NO 7075; 167pp + Sequence Listing; English.
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                                                                                                                                                                                                                                   Ohlsen KL;
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73.8%; Pred. No. 3.9e-137;
live 49; Mismatches 53;
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                                                                                                                                                                                                                                   Bussey
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                                                                    29-DEC-2000; 2000US-0259128P.
20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
                        26-DEC-2001; 2001WO-US049486
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                                                                                                                                                                               (ELIT-) ELITRA PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119
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The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homologue or variant. The second protein or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of apharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition of for developing a disease or disorder in a subject. These are also useful in acreening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein complexes are useful for the manufacture of a medicament of complexes are protein and activity or protein the complexes are protein and activity or protein complexes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New proteins and protein complexes from eukaryotes, useful as targets in drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for the treatment or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).
                                                                                                      G, Kuester B, Schultz J;
Kruse U, Merino A, Bauch A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disease treating protein complex-derived protein #1281.
                                                                                                                                                                                                                                                     OPDYREKYEAEMEEIRNLEIWRAGKAVRSLRPENQ 399
                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 2561; 13pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein complex; drug target; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADK64188 standard; protein; 395 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bauer A, Gavin A, Superti-Furga Marzioch M, Grandi P, Krause R, Michon A, Leutwein C, Rick J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-DEC-2002; 2002EP-00102902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-DEC-2001; 2001EP-00130253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADK64189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1338608-A2.
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Score 1503; DB 7; Length 395; Pred. No. 6.8e-135;

71.8%; 72.9%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                              301 YPLIGKYGMDYMYDACSTTARRGALDWYPIPKNALKPVFODLYESTKNGTETKRSLEFNS 360
                                                                              65 WERADWPKEKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSWKDAVQD 124
                                                                                                                                                                                                                                              GYLYKTTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEATQSL 304
                                                                                                                                                                                                                                                                                                   YPLIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQRSLDYNS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel purified or isolated Cryptococcus neoformans nucleic acid molecule comprising a sequence encoding a polypeptide comprising a sequence not given in the specification. A polymuclectide of the invention has fungicide activity, and may have a use in gene therapy. The nucleic acid is useful for preparing a composition for treating an infection caused by Cryptococcus neoformans. The present sequence represents a C. neoformans sequence of the invention. Note: The sequence data for this patent is not represented in
                                                      9
                                                                                                                                    GWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHGFSPVFKDL
                                                                                                                                                                                        TKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIALGVAIGS
                                                    LRTQAARLICNSRVITAKRTFALATRAAAYSRPAARFVKP-MITTRGLKQINFGGTVETV
                                                                                                                                                                                                        10 LRPMARQL---ATPAVORRSFVAASSMVRATRKAA--VAPTQQQIRGVKTMDFAGHKEQV
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid, useful for preparing a composition for treating an
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9
  56; Indels
                                                                                                                                                                                                                                                                                                                                                                       C. neoformans amino acid sequence SEQ ID NO:3168
                                                                                                                                                                                                                                                                                                                                                         OPDYREKYEAEMEEIRNLEIWRAGKAVRSLRPENQ 399
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection caused by Cryptococcus neoformans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; SEQ ID NO 3168; 136pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fungicide; gene therapy; infection.
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  45;
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 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cryptococcus neoformans.
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N-PSDB; ADB69041.
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homologous nucleic acids required for cellular proliferation

isolate candidate molecules for rational drug discovery programs

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                                                                                               122
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the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.
                                                                                                                          ODGWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHGFSPVFK 182
                                                                                                                                                     DLTKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIALGVAI 242
                                                                                                                                                                                  GSGYLYKTTFEKGVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEATQ 302
                                                                                                                                                                                                  300
                                                                                                                                                                                                               SLYPLIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQRSLDY 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 screening
                                                                                                                                                               design
                                                                         3 ARGFSKALRPMARQLATPAVQRRSFVAASSMVRATRKAAVAPTQQQIRGVKTMDFAGHKE
                                                                                             63 QVWERADWPKEKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSWKDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zyskind JW;
Xu HH;
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                                                                                                                                                                                                                                                                                                                                                     Antisense; prokaryotic essential gene; cell proliferation; drug
                                                    .,
G
                                      Length 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense nucleic acids, useful for identifying proteins
                                                    67; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohlsen Forsyth F
                                                                                                                                                                                                                                                                                                                                        by Prokaryotic essential gene #6503.
                                   ; Score 1421.5; DB 7;
; Pred. No. 4.7e-127;
51; Mismatches 67;
                                                                                                                                                                                                                                           NSQPDYREKYEAEMEEIRNLEIWRAGKAVRSLR 395
                                                                                                                                                                                                                                                   Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                            ABU20976 standard; protein; 347 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malone C,
Carr GJ,
                                    67.9%;
69.2%;
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06-SEP-2001; 2001US-00948933.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072881.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2002; 2002WO-US009107
                                                  272; Conservative
                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                   Bacteroides fragilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-029926/02
                                            Similarity
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                      Sequence 409 AA;
                                                                                                                                                                                                                                                                                                                                        encoded
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Wall D,
                                    Query Match
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the 613 antisense sequences given in the specification where expression of the 613 antisense sequences given in the specification where expression of the 613 antisense sequences given in the specification where expression of the nucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleac acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibitied by the compound that incluences the activity of a gene in an operon required for the activity of a gene in an operon required for the proliferation or the activity of a gene in an operon required for computed for the strain antibitis cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or agene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the compound discovery programs, or for screening homologous nucleic acids are useful for identifying proteins or acreening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target profartoric essential genes modeled acids acids are this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKSWKDAVQDGWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354
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                                                                                        invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۲;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.6%; Score 1100.5; DB 59.9%; Pred. No. 2.3e-96; ive 53; Mismatches 84
    SEQ ID NO 48900; 1766pp; English.
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Matches 206; Conservative
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Claim 25;
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Job time
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5.1.7	Biocceleration
version	- 2006
Core	1993
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OM protein - protein search, using sw model

Run on:

March 22, 2006, 15:27:29 ; Search time 21.1579 Seconds (without alignments) 1828.118 Million cell updates/sec

US-10-797-248A-1 2094

Title: Perfect score: Sequence:

1 MSARGFSKALRPMARQLATP......BIWRAGKAVRSLRPENQKQK 402

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ketol-acid reducto	ketol-acid reducto	ketol-acid reducto	ketol-acid reducto	acetohydroxy acid	ketol-acid reducto	-acid	ketol-acid reducto	alpha-keto-beta-hy	probable ketol-aci	ketol-acid reducto																		
SUMMARIES	ID	JC1428	A24709	T40532	C69644	F70407	AC1694	AB1323	H75044	A96911	G95051	C84032	C97922	D72362	F64492	C90204	A47037	T06825	B86778	S30145	T45681	AD2095	F89997	S35140	C75387	S17180	C81801	F81066	σ	A69059
	BB	-1	Н	7	~	~	~	7	7	N	~	~	~	~	Н	~	~	~	~	-	~	N	~		7		7	~	N	8
	Query Match Length	400	395	404	342	333	331	331	332	337	336	340	340	336	348	335	367	581	340	591	591	331	'n	344	9	σ	m	337	332	333
عد	Owery Match	88.6		71.6			22.9	22.7	22.6	22.5	22.1	22.1	22.1	22.0	21.7	21.7	21.4	21.3	21.3	21.1	21.1	20.8	20.8	20.4	20.4	20.4	20.5	20.2	19.6	19.4
	Score	1856	1503	1499.5	490	481.5	479	475	473	~	462.5	462.5	462.5	461	455	453.5	449	447	446	441	441	436	435	428	427	427	424	424	409.5	406
	Result No.	П	8	æ	4	S	9	7	a 0	Φ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

ketol-acid reducto	ketol-acid reducto	acetolactate synth	ketol-acid reducto	ketol-acid reducto	ketol-acid reducto	ketol-acid reducto	probable ilvC prot	ketol-acid reducto	ketol-acid reducto	hypothetical prote	ketol-acid reducto	ketol-acid reducto	ketol-acid reducto		ketol-acid reducto
G81411	E82634	T35830	C48648	E83059	JC5166	T45415	D70855	H87120	AE2824	D97602	G87511	AB3330	B64561	A71945	ISECKR
7	~	~	Н	N	ч	N	N	~	N	N	~	~	ч	~	н
340	366	332	338	338	333	343	333	333	339	339	339	339	330	330	491
19.1	19.1	18.7	18.5	18.5	17.2	17.1	17.0	17.0	16.7	16.7	16.5	15.9	15.6	15.2	14.6
401	401	391	388	387	361	359	356.5	355	349.5	349.5	345.5	333.5	327	318	306.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1	
	ketol-acid redu N;Alternate nam	ketol-acid reductoisomerase (EC 1.1.1.86) - Neurospora crassa N;Alternate names: alpha-keto-beta-hydroxylacyl reductoisomerase
	C; Species: Neurospora crassa C; Date: 10-Sep-1999 #sequence	ospora crassa 1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
	R;Sista, H.; Bowman,	1426 wan, B. 10 noon
	A; Title: Charac	dene 120, 113-116, 1992 A;Title: Characterization of the ilv-2 gene from Neurospora crassa encoding alpha-keto-b
	A; Reference number:	
	A, Molecule type: DNA	: DNA
	A;Residues: 1-400 <sis></sis>	CONTRACTOR OF THE PROPERTY OF MAY 100
	C;Genetics:	(1700015: GIN (60150W: GD
	A, Gene: ilv-2	
	A; Map position: V	A.Map position: V A.Tatrone: 68/1: 78/3: 170/3: 202/3
_	C, Superfamily:	
	C;Keywords: iso F;87-273/Domain	C;Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrion; oxidoreductase F;87-273/Domain: ketol-acid reductoisomerase homology <kar></kar>
	Query Match Best Local Similarity Matches 349; Conser	88.6%; Score 1856; DB 1; Length 400; milarity 86.8%; Pred. No. 5.2e-134; Conservative 35; Mismatches 14; Indels 4; Gaps 2;
	й т Х	MSARGFSKALRPWARQLATPAVQRRSFVAASSMVRATRKAAVAPTOQQIRGVKTMDFA 58
	da 1 M	: :
	D 65 KO	GHKEQVWERADWPKEKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSW 118
		:
	Qy 119 KI	DGWVPGKNLFEVDEALSRGT
	: Db 121 E	: :
	Qy 179 P	PVFKDLTKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIAL 238
	181 od	
	Oy 239 G	GVAIGSGYLYKTTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEARNETVE 298
	Db 241 GV	GVAVGSGYLYETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVE 300
	Qy 299 EJ	EATOSLYPLIGANGMDWNYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQR 358

301 EATQSLYPLIGAHGMDWMFDACSTTARRGAIDWTPKFKDALKPVFNNLYDSVKNGDERKR 360

g

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359 SLDYNSQPDYREKYEAEMEEIRNLEIWRAGKAVRSLRPENQK 400

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В.G.

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A, Accession: T40532
A, Status: translated from GB/EMBL/DDBJ
A, Residues: 1-404 < PUR-
A, Cross-references: UNIPROT: P78827; UNIPARC: UP1000012D527; EMBL: AL023288; NID: G5832408; §
A, Experimental source: strain 972h-; cosmid c56F2
B, Rawamukai, M.
Bubmitted to the EMBL Data Library, December 1997
A, Description: S, Dombe ILV5 homolog.
A, Description: S, Dombe ILV5 homolog.
A, Accession: T43303
A, Status: translated from GB/EMBL/DDBJ
A, Thile: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A, Reference number: Z17323; MUID: 99162722; PMID: 9501991
A, Status: T42364
A, Status: T42364
A, Reference number: Z17323; MUID: 99162722; PMID: 9501991
A, Status: T42340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-37,'R',39-40,'W',42-91,'S',93-237,'T',239-274,'P',276-296,'P',298-393,'G',:
A;Cross-references: UNIPARC:UPI00001690FE; EMBL:DB9175; NID:g1749557; PIDN:BAA13837.1; Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Pathway: branched-chain amino acid biosynthesis
C.Superfamily: Ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase homc
C;Keywords: isoleucine-valine biosynthesis; isomerase; oxidoreductase
F;88-274/Domain: ketol-acid reductoisomerase homology <KAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTKENVWERSDWPREKIVDYFKNDTLAIIGYGSQGHGQGLNARDQGLNVIVGVRKDGASW 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 KQAIEDGWVPGKTLFPVEEAIKKGSIIMNLLSDAAQTETWPKIAPLITKGKTLYFSHGFS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVAIGSGYLYKTTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDAVQDGWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHGFS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVFKDLTKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIAL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EATOSLYPLIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQR 358
                                       M.H.; Rajandream, M.A.; Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 AVAVGSGFIYQTTFKKEVISDLVGERGCLMGGINGLFLAQYQVLRERGHSPAEAFNETVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHKEQVWERADWPKEKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SARGFSKALRPM-ARQLAT--PAVORRSFVAASSMVRATRKAAVAPTQQQIRGVKTMDFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLDYNSOPDYREKYEAEMEEIRNLEIWRAGKAVRSLRPENOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 71.6%; Score 1499.5; DB 2; Best Local Similarity 71.1%; Pred. No. 8.8e-107; Matches 286; Conservative 56; Mismatches 53;
         C;Accession: T40532; T43303; T42540
R;Purnelle, B.; Goffeau, A.; Wood, V.; Lyne,
submitted to the EMBL Data Library, May 1998
A;Reference number: Z21935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain PR745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene: SPDB:SPBC56F2.12; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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                                                                                                                                        National Section and reductoisomerase (EC 1.1.1.86) ILVS - yeast (Saccharomyces cerevisiae)
NetCol-acid reductoisomerase (EC 1.1.1.86) ILVS - yeast (Saccharomyces cerevisiae)
NyAlternate names acetohydroxyacid reductoisomerase ILVS; protein L9638.7; protein VLR3
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: A24709; S51463
Nucleic Acids Res. 14, 9631-9651, 1986
A;Title: The ILVS gene of Saccharomyces cerevisiae is highly expressed.
A;Accession: A24709
A;Accession: A24709
A;Accession: A24709
A;Molecule type: DNA
A;Residues: 1-395 <-RET>
A;Cross-references: UNIFROT:PO6168; UNIPARC:UPI000012D529; EMBL:X04969; NID:g3826; PIDN: R;Du, Z.
submitted to the EMBL Data Library, December 1994
A;Reference number: S51459
A;Reference number: S51459
A;Reference number: S51459
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T40532
F40532 reductoisomerase (EC 1.1.1.86) [similarity] - fission yeast (Schizosaccharomy
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hor
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A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-395 < DUZ>
A, Cross-references: UNIPARC:UPI000012D529; EMBL:U19102; NID:g609396; PIDN:AAB67753.1; I
C, Genetics:
A, Gene: SGD:LLV5; MIPS:YLR355C
A, Gene: SGD:LLV5; MIPS:YLR355C
A, Map position: 12R
C, Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase hk
C, Reywords: isoleucine-valine biosynthesis; isomerase; mitochondrion; oxidoreductase
F, 81-267/Domain: ketol-acid reductoisomerase homology < KAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WERADWPKEKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSWKDAVQD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHGFSPVFKDL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 TKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIALGVAIGS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YPLIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQRSLDYNS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 LRPMARQL---ATPAVQRRSFVAASSMVRATRKAA--VAPTQQQIRGVKTMDFAGHKEQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 71.8%; Score 1503; DB 1; Best Local Similarity 72.9%; Pred. No. 4.6e-107; Matches 288; Conservative 45; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 OPDYREKYEAEMEEIRNLEIWRAGKAVRSLRPENO 399
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4

Gaps

7;

118

61

241

301

RESULT

Gaps

13;

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Length 333;

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A;Gene: ilvC
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoiso
F;21-203/Domain: ketol-acid reductoisomerase homology «KAR»
                                                                              A;Cross-references: UNIPROT:067289; UNIPARC:UPI0000056582; GB:AE000730; NID:g2983674; Pli
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                   70 WPKEKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSWKDAVQDGWVPG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 KNLFEVDEAISRGTVIMNLLSDAAQSETWP-ALKPQITKGKTLYFSHGFSPVFKDLTKVE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIALGVAIGS--GY 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                6 YDEDASEDILKDKVIAILGYGSQGHAHALNLRDSGLNVIIGLHEGSRSREKAKADGF---
                                                                                                                                                                                                                                                                                         23.0%; Score 481.5; DB 2; 33.3%; Pred. No. 3.7e-29; tive 72; Mismatches 135;
                                                                                                                                                                                                                                                                                                                         Local Similarity 33.39
                            :ype: DNA
1-333 <AQF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: AC1694
                         A; Molecule type:
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Matches 110;
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                                                                                                                                            C;Genetics:
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ketol-acid reductoisomerase ilvC - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
C;Accession: C69644
E;Kunst, F: Ogasawara, N: Moszer, I:; Albertini, A.M.; Alloni, G:; Azevedo, V.; Berter
C; Broi, S.; Brounillet, S.; Brucehi, C.V; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferreri, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hibbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A,Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Msudel,
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A,Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowaka, A.; Sero,
A,Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowaka, A.; Sero,
A,Authors: Voshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama,
A,Authors: Voshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama,
A,Accession: C69644
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Rolecule type: DNA
A;Residues: 1-342 cKUN>
A;Residu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: ilvC
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type;,ketol-acid reductoisq
F;21-202/Domain: ketol-acid reductoisomerase homology <KAR>
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C,Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Oct-2004
C,Accession: F70407
R,Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Atle: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70407
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -ETTPKEETETDIJFGEQAVLCGGLSALVKAGFETLTEAGYQPELAYFECLHE-LKLIVDL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308 IGANGMDWMYEACSTTARRGAIDWSPRFKDA-LKPVFNQLYDSVKDGSETQRSLDYN--S 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFEVDEAISRGTVIMNLLSDAAQSETWPA-LKPQITKGKTLYFSHGFSPVFKDLTKVEVP
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23.4%; Score 490; DB 2; Length 34;
Best Local Similarity 36.7%; Pred. No. 8.6e-30;
Matches 122; Conservative 68; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acetohydroxy acid isomeroreductase - Aquifex aeolicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
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Vidiaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H., J. Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Teterence number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1694
A;Actus: preliminary
A;Molecule type: DNA
A;Residues: I-331 GGIA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ketol-acid reductoison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ketol-acid reductoisomerase (acetohydroxy-acid isomeroreductase) homolog ilvC [imported]
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UP10000CC759; GB:AL592022; PIDN:CAC97323.1; PID:g16414607; A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10,
                                         ::|||::| :||:|::|::|
179 VIETTFKEETETDLFGEGWVLCGGVTALIKAGFETLVNAGYQPEVAYFECLHE-LKLIVD 237
LYKTTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEATQSLYP 306
                                                                                                                                                          LIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQRSLDYNSQP 366
                                                                                                                                                                                                                                     238 LIYEHGISGMRYSISDTAKYGDVTRGERIYKVVKPVMEKTLEBIQKGBFAREWILENKAG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187
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C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type;
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Clacesion: H75044
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struct
A;Reference number: A75001
A;Reference number: A75001
A;Accession: H75044
A;Accession: H75044
A;Reference number: A75001
A;Accession: H7504
A;Residues: 1-332 ckAW>
A;Residues: 1-332 ckAW>
A;Residues: 1-332 ckAW>
A;Residues: UNIPROT:Q9UZO9; UNIPARC:UPI000003453B; GB:AJ248287; GB:AL096836; NID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asolation reductoisomerase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004
C;Accession: A96911
R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J; Bacteriol. 183, 4823-4838, 2001
A;Reference number: A96900; MulD:21359325; PMID:21359325
A;Accession: A96911
A;Status: preliminary
A;Status: Day
A;Status: Day
A;Status: Day
A;Status: Day
A;Residues: 1-337 < **MID:2137** A;Accession A;Acc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoison F;24-206/Domain: ketol-acid reductoisomerase homology <KAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 YVDVIMVAPKSPGKRVREKYLEGFGVPALVAVYQDYTGNAKDLALAMAKAIGCTRAGVI- 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KITFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEATQSLYPLI 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 GANGMDWMYEACSTTARRGAIDWSPR-FKDALKPVFNQLYDSVKDGSETQRSLDYNSQPD 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 YERGFTGMLKAVSDTAKYGGLTVGPKVIDDHVKENMKKPAERVRSG---EFAKEWISKAD 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 EKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSWKDAVQDGWVPGKNL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 FEVDEAISRGTVIMNLLSDAAQSETW-PALKPQITKGKTLYFSHGFSPVFKDLTKVEVPT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
ketol-acid reductoisomerase (ilvc) PAB0889 - Pyrococcus abyssi (strain Orsay)
                                       C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 EVSMDILKDKTVAVIGYGNQGEAQAKNNRDSGVHVILGIRPSGSSWKRAEKDGF---EV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 22.6%; Score 473; DB 2; Length 33: Best Local Similarity 35.4%; Pred. No. 1.6e-28; Matches 116; Conservative 71; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 22.5%; Score 472; DB 2; Length 33° Best Local Similarity 34.2%; Pred. No. 2e-28; Matches 115; Conservative 65; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         368 -YREKYEAEMEEIRNLEIWRAGKAVRSL 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 KASEVLEELMKPIEEHEIEKVGRFIRKM 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Experimental source: strain Orsay C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: ilvC; PAB0889
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Ketol-acid reductoisomerase (acetohydroxy-acid isomeroreductase) homolog ilvC [imported]
C,Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #text_change 05-Oct-2004
C;Accession: AB1323
R;Glaser, P:; Frangeul, L:; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.; Dominguez-Bernal, G; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D:; Jones, L.M.; Karst, U.
Science. 294, 849-682, 2001
A,Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Varquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Fitle: Comparative genomics of Listeria species.
A;Fitle: Comparative genomics of Listeria species.
A;Fitle: Comparative Genomics of Listeria Species.
A;Focession: AB1323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-331 <GLA>
A;Cross-references: UNIPARC:UPI0000054FF8; GB:NC_003210; PIDN:CAD00064.1; PID:gl6411439; A;Geneerian source: strain EGD-e
C;Geneerics:
A;Gene: ilvC
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisc
                                                                              EVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIALGVAIGS--G 245
                                                                                                                                                                                                246 YLYKTIFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEATQSLY 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 PLIGANGMOWMYEACSTTARRGAIDWSPRFKDA-LKPVFNQLYDSVKDGSETQRSLDYNS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 YFKD-----DTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSWKDAVQDGWVP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 GKNLFEVDEAISRGTVIMNLLSDAAQSETWP-ALKPQITKGKTLYFSHGFSPVFKDLTKV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 EVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIALGVAIGS--G 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 YLYKTTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEATQSLY 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 QPDYREKYEAEMEEIRNLEIWRAGKAVRSLRP 396
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296 N-GFKEFHRMRKEQ-QGHQIEKVGAELREMMP 325
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R.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira. Mucleic Acids Res. 28, 4317-4331, 2000
ArItle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and Akeference-number: A83650; WUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cipaces (27-001-2004)

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A;Cross-references: UNIPROT:Q9K8E7; UNIPARC:UPI000012D53B; GB:AP001517; GB:BA000004; NID
A;Experimental source: strain C-125
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C.Species: Streptococcus pneumoniae
C.Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 05-Oct-2004
                                                                                                                                                                                                               ketol-acid reductoisomerase ilvC [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLALIGYGSQCHGQGLNLRDNGLNVIIGVRKDGKSWKDAVQDGWVPGKNLFEVDEAISRG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIALGVAIGSGY--LYKTTFEKEVYSD 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 TVIMNLLSDAAQSETWP-ALKPQITKGKTLYFSHGFSPVFKDLTKVEVPTDVDVILCAPK 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYGERGCIMGGIHGMFLAQYEVLRERGHSPSBAFNETVEEATQSLYPLIGANGMDWMYEA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 CSTTARRGAIDWSPRFKDA-LKPVFNQLYDSVKDGS-----ETQRSLDYNSQPDYREK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004
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       ---DYKAGRPKLTAYREQAANLEIEKVGAELRKAMP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Pred. No. 1.1e-27; 57; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 22.1%; Score 462.5; Best Local Similarity 35.4%; Pred. No. 1.1 Matches 115; Conservative 57; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                       C, Accession: C84032
                                          290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 05-Oct-2004
C;Accession: G9501
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Authors: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisd
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A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0447
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisc
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ketol-acid reductoisomerase [imported] - Streptococcus pneumoniae (strain TIGR4)
                                                                                                                                DEAISRGTVIMNLLSDAAQSETWPA-LKPQITKGKTLYFSHGFSPVFKDLTKVEVPTDVD 194
                                                                                                                                                                                                                                                                                                                EKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEATQSLYPLIGANG 312
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                                                                                                                                                                               VILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIALGVAIG--SGYLYKTTF 252
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   LEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSWKDAVQDGWVPGKNLFEV 135
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                                   232 VDLIYEGGFKKMRQSISNTAEYGDYVSGPRVITEQVKENMKAVLADIQNGKFANDFVN-- 289
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Matches 122; Conserv
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A,Status: preliminary
A,Molecule type: DNA
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C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 05-Oct-2004
C;Accession: C90204
R;She, Q:; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-VJong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
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C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisd
C;Reywords: isomerase; oxidoreductase
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D72362
ketol-acid reductoisomerase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 05-Oct-2004
C;Accession: D72362
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Gene: TM0550
;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisc
;21-203/Domain: ketol-acid reductoisomerase homology <KAR>
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A;Residues: 1-336 <ARN>
A;Cross-references: UNIPROT:Q9WZ20; UNIPARC:UPI000012D560; GB:AE001730; GB:AE000512;
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                                                          22.1%; Score 462.5; DB 2; Length 36.3%; Pred. No. 1.1e-27; ive 54; Mismatches 131; Indels
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                                                                                                  Matches 122; Conservative
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                                                                               Best Local Similarity
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Recol-acid reductoisomerase (EC 1.1.1.86) - Methanococcus jannaschii (Species: Methanococcus jannaschii) (Species: Methanococcus jannaschii) (Species: Methanococcus jannaschii) (Species: Methanococcus jannaschii) (Species: Methors: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoison C;Keywords: isoleucine-valine biosynthesis; isomerase; oxidoreductase
F;39-221/Domain: ketol-acid reductoisomerase homology <KAR>
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C;Genetics:
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                                                                                                                                307 LIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQRSLDY--NS 364
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179 VIETTFKEETETDLFGEQAVLCGGVTALIKAGFETLVDAGYQPEIAYFECLNE-LKLIVD 237
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                                                                                                                                                                                                                             70 WPKBKILEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSWKDAVQDGWVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 VDLÍYQKGLQGMWENVSNTÁBYGGLTRRARVINEBSRKAMKBILKEIQDGRFAKEWSLE-
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Submitted to GenBank, April 2001
A, Description: Sulfolobus solfataricus complete genome.
A, Reference number: A99139
A, Reference number: A99139
A, Accession: C904
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-335 < KUR>
A, Fesidues: 1-335 < KUR>
A, Cross-references: UNIPROT: Q9UWX9; UNIPARC: UP1000012D50D; GB: AE006641; NID: g13813740; E C, Generics:
A, Generics:
A, Generics:
A, Generics:
C, Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoise
                                                                                                                                                                                                                                                                                                        76 LEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSWKDAVQDGWVPGKNLFEV 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 MDWMYEACSTTARRG-----AIDWS--PRFKDALKPV------FNQLYDSVK 351
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                                                                                                                                                                                                                                                                           33;
                                                                                                                                                                                                                                  Query Match 21.7%; Score 453.5; DB 2; Length 335; Best Local Similarity 35.7%; Pred. No. 5.1e-27; Matches 111; Conservative 60; Mismatches 107; Indels 33;
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Search completed: March 22, 2006, 15:34:32 Job time : 22.1579 secs Inis Page Blank (uspic)

1 جمر

OM protein - protein search, using sw model

March 22, 2006, 15:21:27; Search time 125.94 Seconds (without alignments) 2252.046 Million cell updates/sec Run on:

US-10-797-248A-1 2094 1 MSARGFSKALRPWARQLATP.......EIWRAGKAVRSLRPENQKQK 402 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2166443 Total number of hits satisfying chosen parameters:

2166443 segs, 705528306 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q52f28 magnaporthe	P38674 neurospora	O4hy40 qibberella				-	Q6cy71 kluyveromyc	Q59ww5 candida alb	Q59xr8 candida alb	Q6fxg6 candida gla	saccharc		P78827 schizosacch	Q02340 saccharomyc	Q75cw4 ashbya goss		_	_			Q519j3 bacteroides	Q8a612 bacteroides			_		_	P37253 bacillus su	O67289 aquifex aeo	ro-
SUMMARIES	ID	Q52F28 MAGGR	ILVS NEUCR	Q4HY40 GIBZE	Q4WYW4_ASPFU	Q5BAA4_EMENI	Q6CAF8_YARLI	Q6BLZ4_DEBHA	Q6CY71_KLULA	Q59WW5 CANAL	Q59XR8 CANAL	Q6FXG6_CANGA	ILV5_YEAST	Q02341_YEAST	ILV5_SCHPO	Q02340_YEAST	Q75CW4_ASHGO	Q55QW8_CRYNE	Q5KFA0_CRYNE	Q96VZ5_CRYNE	Q4P572_USTMA	094135_9FUNG	Q5L9J3_BACFN	Q8A612_BACTN	Q64PT1_BACFR	Q847R5_ASTYP	Q5KWJ2 GEOKA	Q8RL86 BACST	ILVC PYRFU	1LVC_BACSU	ILVC_AQUAE	ILVC_LISIN .
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de	Query Match	99.4	89.8	88.9	80.0	79.9	75.5	73.6	73.1	72.9	72.8	71.9	71.8	71.7	71.6	71.1	70.1	68.5	68.5	9.19	59.8	53.4	52.7	52.6	52.6	49.8	24.4	24.2	23.6	23.4	23.0	22.9
	Score	2081	1881	1861.5	1675	1673	1581.5	1542	1530	1526.5	1524.5	1505.5		1501	1499.5	1489	1467.5	1433.5	1433.5	1416.5	1253	1119	1102.5	1102	1100.5	1043	510.5	507	494	490	481.5	479
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Q71y36 listeria mo Q73bal bacillus ce Q61hf4 bacillus th Q63dx9 bacillus th Q82tel pyrobaculum Q8y580 listeria mo Q81g13 bacillus ce Q9uzQ9 pyrococcus Q7mv0 clostridium Q5wen2 bacillus cl Q65g17 bacillus cl Q61t69 bacillus li Q61t69 bacillus an Q51xy0 streptococc	Q5m2f2 streptococc
11.VC LISWF 11.VCT BACC1 60411.F4 BACHK 0633DX9_BACCZ 11.VC_LISWO 11.VCT_LISWO 11.VCT_LISWO 11.VCT_CLOAB 11.VCT_CLOAB 11.VCT_CLOAB 0598702 BACSK 065617_BACLD 11.VCT_BACLD	Q5M2F2_STRT2
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ALIGNMENTS

RESULT 1

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100	ID 052F28 MAGGR PRELIMINARY: PRT: 400 AA
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3 5	-SEP-2005 (Irambirel. -SEP-2005 (TrEMBirel.
E S	l protein.
SO	Ontrames-modified ::) Magnaporthe grises 70-15.
ဗ	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
8	Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
N O	NCBI_TaxID=242507;
КР	NUCLEOTIDE SEQUENCE.
22	STRAIN=70-15;
&	Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
8 8	Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
¥ 8	Arachchi H., Armoruster U., Bachantsang P., Baldwin U., Barry A., Ravil T. Blitshstevn B. Bloom T. Bloom J. Bornelswekiv I.
8	Borowsky M., Boukhqalter B., Brunache A., Butler J., Calixte N.,
Æ	Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
R.	Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
S :	David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
£ 6	Dricken I Barina N. Park Bricken I Bagels K.,
8	Fitzgerald M., Folev K., Gage D., Galagan J., Gearin G., Gnerre S.,
R3	Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
R.	Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
Z G	Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
5 2	valle D., Johns C., Admal M., Kamar A., Kamyyssells M., Karlsson E., Kells C., Kien A., Kisner P., Kodira C., Kulbokas R., Labutti K
Æ	Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
8	A Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
¥ 6	היבותם איז, Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J., איזיים איזיים
5 ₹	McCarthy M., McGonough S., Mcchee T., Meldrim J., Meneus L.,
Æ	Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
¥ :	Mozes J., Mulrain L., Munson G., Naylor J., Newes C., Nguyen C.,
X 5	Nguyen N., Nguyen T., Nicol K., Nielsen C., Nizzari M., Norbu C., Norbi M. O'donnell D. Okosino O'losmi C. Omotonko D
2	K., Osman S.,
R.	
A 6	Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
5 S	Sheridan J. Sherba N., Shi J., Smirnov S., Smith C., Soudnez C.
Æ	Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
8:3	Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
\$ &	Tenzing F., Testaye S., Ineodore J., Thoulutsang Y., Topham K., Towey S., Tsamla T. Tsomo N. Valles D. Vassiliev H
8	Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
8 8	Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S., Yang S., Yang X., Yeager S., Yee B., Young G., Zainoun J., Zembeck L.,
Z.	Zimmer A., Zody M., Lander E.;

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MEDLINE=93013010; PubMed=1398116; DOI=10.1016/0378-1119(92)90018-K;
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                                                                                                                                                                                                                                                                                                                                                                                          AVQDGWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYPSHGFSPV 180
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P38674; Q7RVD5; Q8X019;
01-FEB-1995 (Rel. 31, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Ketol-acid reductoisomerase, mitochondrial precursor (EC 1.11.1.86)
(Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil
                                                                                                                               CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                       DB 2; Length 400;
                                                                                                                                                                                                                                                                            0; Indels
                                         STRAIN=70-15;
Dean R., Mitchell T., Brown D., Pan H., Thon M.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBU databases.
         to the EMBL/GenBank/DDBJ databases.
                                                                                                                      (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 400 AA; 44723 MW; 4C89B9E1495B6D75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYNSOPDYREKYEAEMEEIRNLEIWRAGKAVRSLRPENOK 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 DYNSQPDYREKYBAEMEEIRNLEIWRAGKAVRSLRPENQK 400
                                                                                                                                                    preliminary data.

EMBL; AACUO1000121; EAAS6157.1; -; Genomic_DNA.

InterPro; IPR000506; AcH isomrdctse.

InterPro; IPR009014; Transketo_C_like.

Pfam; PF01450; IlvC; 1.

TIGRFAMS; TIGR00465; ilvC; 1.
                                                                                                                                                                                                                                                      Score 2081; DB 2;
Pred. No. 6e-141;
 grisea.";
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Name=ilv-2; ORFNames=B11H24.150, NCU03608;
 Magnaporthe
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NUCLEOTIDE SEQUENCE.
STRAIN=70-15;
Zhu H., Blackmon B.;
Submitted (OCT-2003) t
 "The genome sequence
           Submitted (OCT-2003)
                                                                                                                                                                                                                                                                  Similarity
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                                NUCLEOTIDE SEQUENCE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=74-0R23-1A / FGSC 987;

NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=74-0R23-1A / FGSC 987;

MADLINE=25598136; PubMed=12712197; DOI=10.1038/nature01554;

A dalagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

A dalefe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,

B likins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,

A dulagan J.E., Garenberg P., Roy A., Foley K., Newse H.-W., Staben C.,

Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,

A stange-Thomann N., Barrett R., Gnerre S., Kamal M., Kamvysselis M.,

Rasmussen C., Metzenberg B.L., Perkins D.D., Kroken S., Cogoni C.,

Maccil E., Bielke C., Rudd S., Frishman D., Krystofova S.,

Rasmussen C., Metzenberg R.L., Derkins D.D., Kroken S.,

A varden O., Plamann M., Seiler S., Dunlap J.C., Radford A., Aramayo R.,

Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,

Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,

Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,

Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,

Natvig C., Catcherie S., Linker S., Nusbaum C., Birren B.W.;

Nature 422:859-868(1003).

- Grallytity: (2R, 23, -dihydroxy-3-methylbutanoate + NADPH.

C. CATALYTIC ACTIVITY: (2R, 3R) -2, 3-dihydroxy-3-methylpentanoate + NADPH.

C. CATALYTIC ACTIVITY: (2R, 3R) -2, 3-dihydroxy-3-methylpentanoate + NADPH.
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-!- PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine
Sista H., Bowman B.; "Characterization of the ilv-2 gene from Neurospora crassa encoding alpha-keto-beta-hydroxylacyl reductoisomerase."; gene 120:115-118(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- COFACTOR: Magnesium.
-1- PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-
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-!- SUBCELLULAR LOCATION: Mitochondrial.
-!- SIMILARITY: Belongs to the ketol-acid reductoisomerase family.
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Pfam, PF0456; .lvc; 1.
TIGREAMS, TIGR00465; ilvc; 1.
Amino-acid biosynthesis; Branched-chain amino acid biosynthesis;
Amono-acid biosynthesis; Branched-chain amino acid biosynthesis;
Magnesium; Mitochondrion; NADP; Oxidoreductase; Transit peptide.
TRANSIT 1 26 Mitochondrion (Potential).
CHAIN ... 99 NADP (Potential).
                                                                                                                                                                                                                                                                                                             Mannhaupt G., Montrone C., Haase D., Mewes H.-W., Aign V.,
Hoheisel J.D., Fartmann B., Nyakatura G., Kempken F., Maier J.,
                                                                                                                                                                                                                                                                                                                                                                                      Schulte U., "What's in the genome of a filamentous fungus? Analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1881; DB 1; Length 402;
                                                                                                                                                                                                                           STRAIN=74-0R23-1A / FGSC 987;
MEDLINE=22542210; PubMed=12655011; DOI=10.1093/nar/gkg293;
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246F795898D2A174 CRC64;
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EMBL; AL670005; CAD21284.1; -; Genomic DNA.
EMBL; AABX01000270; EAA32099.1; -; Genomic_DNA.
HSSP; Q9HVA2; INP3.
                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurospora genome sequence.";
Nucleic Acids Res. 31:1944-1954(2003).
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                                                                                                                                                                                                                                                                                                          Arachenia B., Niusbaum C., Abouelleil A., Allen N., Anderson S., Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L., Burch H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L., Buckhgalter B., Butler J., Calvo S. E., Camarata J., Chang J., Chang J., Cholymore A., Cook P., Cocke P., Corum B., DeArellano K., Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R., Erickson J., Farco S., Ferreira P., FitzGerald M., Gage D., Galagan J., Ragopian D., Hagos B., Hall J., Horton L., Hulme W., Hafez N., Hagos B., Hall J., Horton L., Hulme W., Iliev I., Antiev T., Lindelad-Toh K., Liu G., Lui A., Mall J., Marcien C., Macdonald P., Major J., Manning J., Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L., Micola V., Mirchy T., Naylor J., Manning J., Milsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D., Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S., Roman J., Schauer S., Schubback R., Seaman S., Severy P., Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M., Talamas J., Tesfaye S., Theodore J., Topham K., Travers M., Waman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M., Lander E.,
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                                                    PVFKDLTKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIAL
                                                                                                                                                                                                        PVFKDLTKVEVPTDVDV1LVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEKAVAL
                                    1 MSARGFSKALRPMARQLATPAVQRRSFVAASSMVRAT--RKAAVAPTQQQIRGVKTMDFA
                                                                                       GHKEQVWERADWPKEKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSW
                                                                                                                                       KDAVQDGWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHGFS
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13-SEP-2006 (TrEMBLrel. 31, Last annotation update)
11-US NEUCR Ketol-acid reductoisomerase, mitochondrial (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil
               2;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
87.6%; Pred. No. 1.4e-126;
tive 35; Mismatches 13; Indels
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Q4HY40;
              Matches 352; Conservative
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 Best Local Similarity
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A Mierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,

A Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,

Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,

Raman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,

Bosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,

Coldman G.H., Gomi K., Griffith Jones S., Gwilliam R., Haas B.,

A Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,

Raller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,

Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,

A Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,

A Majoros W.H., May G.S., Murphy L., O'Neil S., Paulsen I.,

Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,

Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,

Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,

Rabbinowitsch E., Salaberg S.L., Sanchez M.,

Ronning C.M., Rutter S., Salaberg S.L., Sanchez M.,

Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares S.,
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                               entry which is
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(FEB-2004) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
                            -!- CAUTION: The sequence shown here is derived f
EMBL/GenBank/DDBJ whole genome shotgun (WGS)
                                                                                                                                                                                                                                          88.9%; Score 1861.5; DB 2 88.1%; Pred. No. 3.5e-125;
                                                                                                                  EMBL; AACM01000419; EAA67345.1; -; Genomic_DNA
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Matches 357; Conservative
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Q4WYW4;
                                                                                        preliminary data.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EATQSLYPLIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQR 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 DSKETVYERADWPREKLOEYFKNDTLALIGYGSQCHGQGLNLRDQGLNVIVGVRKDGASW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVAVGSGXLYETTFEKEVYSDLYGERGCLMGGIHGMFLAOYEVLRERGHSPSEAFNETVE
Takeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J., White O., Woodward J., Yu J.-H., Fraser C., Galagan J.B., Asai K., Machida M., Hall N., Barrell B., Denning D.W., "Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergilus funiqueus.", pathogenic and allergenic filamentous fungus Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHKEQVWERADWPKEKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDAVQDGWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVPKDLTKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSARGFSKALRPMARQLATPAVQRRSFVAASSMVRATRKAA--VAPTQQQIRGVKTMDFA
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Birrain-FGSC A4;
Birrain B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
Boukhgalter B., Burler J., Calvo S.E., Camarata J., Chang J.,
Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
Erickson J., Paro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, Emericella.
                                                                                                                                                                                                                                                                                                                                 Length 508;
                                                                                                                                                                                                                                                                                                                            80.0%; Score 1675; DB 2; Length 5 79.4%; Pred. No. 1.1e-111; ive 42; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508 AA; 56353 MW; 09C99AB04D9D92EC CRC64;
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Last annotation update)
                                                                                                                                                                                                   preliminary data.
EMBL; AAHF01000002; EAL92139.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 79.48
Matches 319; Conservative
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QSBAA4;
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                                                                                                                                                                                                                                                         Isomerase.
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                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETVEEATQSLYPLIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGS 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 AIAMGVAVGSGYLYETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFN
Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L., Mihova T., Menga V., Murphy T., Naylor J., Nguyen C., Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D., Oliver J., Reterson K., Phunkhang P., Pierre N., Purcell S., Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P., Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S., Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M., Talamas J., Tesfaye S., Theodore J., Topham K., Travers M., Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B., Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M., Lander E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKSWKDAVQDGWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGFSPVFKDLTKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 ETVEEATQSLYPLIGANGMDMMYAACSTTARRGAIDWSSRFKDNLKPLFNELYDSVRDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSARGFSKALR----PMARQLATPAVQRRSF--VAASSMVRATRKAAVAPTQQQIRGVKT
                                                                                                                                                                                                                                                                                                                                                       "Genome Sequence of Aspergillus nidulans.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AACD1000043; EAA64631.1; -; Genomic DNA.
GO:0004455; F:ketol-acid reductoisomerase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
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Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Yarrowia lipolytica chromosome D of strain CLIB99 of Yarrowia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.9%; Score 1673; DB 2; Length 400; 78.8%; Pred. No. 1.2e-111; ive 38; Mismatches 36; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BTORSLDYNSOKDYREKYEKEMOEIRDLEIWRAGKAVRSLRPENOK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ll protein.
400 AA; 44354 MW; F76A7F2A5AB65FA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
STRAIN=CLIB 122 / E 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro, IPR000506; AcH_isomrdctse. Pfam; PF01450; IlvC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMS; TIGR00465; ilvC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 78.8
hes 320; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4952;
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FGGMDEIVHERADWPREKTLEYFKNDTLALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGA 116
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                                                                                                                    A pujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A pujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Goffard N., Frangeul L., Aajele M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Despons L., Fabre E., Faithead C., Ferry-Dunazet H., Groppi A.,
Hantraye F., Hennequin C., Terry-Dunazet H., Groppi A.,
A Micaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropulos O.,
A Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropulos O.,
A Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Seniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
A Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
A Wincker P., Souciet J.-L.,
T., "Genome evolution in yeasts.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 VEEATQSLYPLIGKYGMDYMYDACSTTARRGALDWYPRFKDALKPVFNDLYESVKNGTET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297 VEEATQSLYPLIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSARGFSKALRPMARQLATPAVQRRSFVAASSMVRATR----KAAVAPTQQQIRGVKTMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSIRNASIRMARMASNNA--AKQVASKRALSALANAARPVVARKSIAPA--AARGVKTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FACHKEQVWERADWPKEKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWXDAVQDGWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSPVFKDLTKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALGVAIGSGYLYKTTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016853; F:isomerase activity; ĪEA.
GO; GO:0004455; F:ketol-acid reductoisomerase activity; IEA.
GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 399;
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25-0cT-2004 (TrEMBLrel. 28, Last sequence update)
25-0cT-2004 (TrEMBLrel. 28, Last annotation update)
Kluyveromyces lactis strain NRRL Y-1140 chromosome A of 1140 of Kluyveromyces lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44352 MW; 53D67F203BD09113 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.6%; Score 1542; DB 2; 74.2%; Pred. No. 2.9e-102; ive 44; Mismatches 52;
                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CR382138; CAG89118.1; -; Genomic_DNA. D:0016853; F:isomerase activity; ĪEA.
                                                                              STRAIN=ATCC 36239 / CBS 767;
PubMed=15229592; DOI=10.1038/nature02579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000506; AcH_isomrdctse.
Pfam; PF01450; IlvC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome; Isomerase.
SEQUENCE 399 AA; 44352 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIGREAMS; TIGRO0465; ilvC; 1.
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QCCY71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 74.2%
Matches 299; Conservative
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PubMed=15229592; DOI=10.1038/nature02579;
A Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffeard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
Swennen D., Tekaia F., Mesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Mayer M., Zivanovic Y., Bolotin-Pukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0004455; F:ketol-acid reductoisomerase activity; IEA.
GO:0016491; F:oxidoreductase activity; IEA.
GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to ca|CA1983|CaILVS Candida albicans CaILVS ketol-acid
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OrderedLocusNames=DEHA0F10483g;
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Pfam; PF01450; IlvC; 1.
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Q6BLZ4;
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SEQUENCE 398 AA;
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                                                                     NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;

Pubmed=15229592; DDI=10.1038/nature02579;

Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

Lafontaine I., de Montigmy J., Marck C., Neuveglise C., Talla E.,

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Astray S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

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Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

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Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,

Swennen D., Tekais F., Wesolowski-Louvel M., Westhof E., Wirth B.,

Sennen D., Tekais F., Wesolowski-Louvel M., Westhof E., Wirth B.,

Seniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,

Mincker P., Souciet J.-L.;

"Genome evolution in yeasts.";
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Nature 430.35-44 (2004).

EMBL; CR382121; CAH02706.1; -; Genomic DNA.

GO; GO:0004455; F:ketol-acid reductoisomerase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
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                   Kludyveromyces lactis (reast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetacese; Kluyveromyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               7634BEC037ABAA9B CRC64;
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Pfam; PF01450; IlvC; 1.
OrderedLocusNames=KLLA0A02673g;
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               Kluyveromyces lactis (Yeast)
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SEQUENCE 397 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-SC5314;
Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
Jones T., Scherer S., Agabian N.;
"Annotation of the Genome of Candida albicans.";
submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
                                                                                                                                                                                                                                                                  STRAIN=SC5314;
PubMed=15123810; DOI=10.1073/pnas.0401648101;
Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
Davis R.W., Scherer S.;
                                                                                                                                 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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73.8%; Pred. No. 3.8e-101;
.ive 49; Mismatches 53; Indels
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Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update) 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
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Likely mitochondrial ketol-acid reductoisomerase.
Name=ILV5; ORFNames=CaO19.7733;
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                                                                                                        Candida albicans SC5314.
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                                                                                                       PubMed=15123810; DOI=10.1073/pnas.0401648101;
Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
Davis R.W., Scherer S.,
"The diploid genome sequence of Candida albicans.";
                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
CORT_TAXID=237561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Candida glabrata strain CBS138 chromosome B complete sequence.
OrderediccusNames=CAGL0B03047g;
Candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
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                                                                                                                                                                                                                              Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O. Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W., Jones T., Scherer S., Agabian N.;
"Annotation of the Genome of Candida albicans.";
Submitted (APR-2004) to the EMBL/Genbank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                             "The diploid genome sequence of Candida albicans.";
Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
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EMBL; AACQ01000106; EAK95225.1; -; Genomic_DNA.
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Name=ILV5; ORFNames=CaO19.88;
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QEFXGE;
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            Candida albicans SC5314.
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Dujon B., Sherman D., Fischer G., Durrens P., Carla B.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
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Zeniou-Meyer M., Zivanovic Y., Bolotin-Pukuhara M., Thierry A.,
A Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
A Wincker P., Souciet J.-L.,
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GO; GO:0004455; F:ketol-acid reductoisomerase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:000982; P:branched chain family amino acid biosynthesis; IEA.
InterPro; IPR000505; AcH_isomrdctse.
Pfam; PF01450; IlvC; 1.
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01-07N-1988 (Rel. 06, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Ketol-acid reductolsomerase, mitochondrial precursor (EC 1.11.86)
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBL_TaxID=5478;
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                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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PubMed=15229592; DOI=10.1038/nature02579;
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"Genome evolution in yeasts.";
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MEDLINE-97313267; Pubbed=9169871;
Ansorge W., Benedror M., Delius H., Dubois E.,
Ansorge W., Benes V., Brueckner M., Delius H., Dubois E.,
Ansorge W., Benes V., Brueckner M., Delius H., Dubois E.,
A Duesterhoeft A., Enlian K., Floeth M., Goffeau A., Hebling U.,
Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K.,
Koetter P., Louis E.J., Messenguy F., Mewes H.-W., Miosga T.,
Mostl D., Meller-Auer S., Nentwich U., Obermater B., Piravandi E.,
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Rinke M., Rose M., Scharfe M., Scherens B., Scholler P., Schwager C.,
Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenbol M.,
Verhasselt P., Vierendeels F., Voet M., Volckaert G., Voss H.,
Wambutt R., Wedler E., Wedler H., Zimmermann F.K., Zollner A.,
Hani J., Hoheisel J.D.;
Hani J., Hoheisel J.D.;
Marker, A., Ander C., Medler M., Meller M., Meller M.,
Marker, A., Ander M., Meller M., Meller M., Meller M.,
Marker, A., Ander M., Meller M., Me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97121404; PubMed=8962070; DOI=10.1073/pnas.93.25.14440; Shevchenko A., Jensen O.N., Podtelejnikov A.V., Sagliocco F., Wilm M., Vorm O., Mortensen P., Shevchenko A., Boucherie H., Mann M.; Linking genome and proteome by mass spectrometry: large-scale identification of yeast proteins from two dimensional gels."; Proc. Natl. Acad. Sci. U.S.A. 93:14440-14445(1996).

-!- CATALYTIC ACTIVITY: (R.-2, 3-dihydroxy-3-methylbutanoate + NADP(+) = (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-isoleucine from 2-oxobutanoate: step 2.
PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from pyruvate: step 2.
SUBCELLULAR LOCATION: Mitochondrial.
SIMILARITY: Belongs to the ketol-acid reductoisomerase family.
(Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil
                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
MEDILINE=87117524; PubMed=3027658;
MEDILINE=870.0..., Holmberg S.;
"The ILVS gene of Saccharomyces cerevisiae is highly expressed.";
Nucleic Acids Res. 14:9631-9651(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=S288C;
MEDLINE=95203288; PubMed=7895733;
Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B Volpe T., Warner J.R., McLaughlin C.S.;
"Protein identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NADP(+) = (S)-2-hydroxy-2-ethyl-3-oxobutanoate + NADPH
                                                  Name=ILV5; OrderedLocusNames=YLR355C; ORFNames=L9638.7;
                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Sacch
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                          [2]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X04969; CAA28643.1; -; Genomic_DNA
EMBL; U19102; AAB67753.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Electrophoresis 15:1466-1486(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN SEQUENCE OF 166-174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COFACTOR: Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 387:87-90(1997).
                                                                                                                                                                                                                                                                                                                                                                  / AB972;
                              reductoisomerase)
                                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                          STRAIN=S288C
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IntAct; P06168; -. GermOnline; 142419; -. SWISS-2DPAGE; P06168; YEAST.

A24709; A24709

HSSP;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|||||||:||||:||||::|
61 YERADWPREKLLDYFKUNDTFALIGYGSQGYGQGLNIRDNGLNVIIGVRKDGASWKAAIED 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GYVYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVERATQSL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 YPLIGKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFODLYESTKNGTETKRSLEFNS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 GWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHGFSPVFKDL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 YPLIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQRSLDYNS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 TKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIALGVAIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 LRPMARQL---ATPAVQRRSFVAASSMVRATRKAA--VAPTQQQIRGVKTMDFAGHKEQV
SGD; S000004347; ILVS.
GO; GO:0042645; C:mitochondrial nucleoid; IDA.
GO; GO:0042645; C:mitochondrial nucleoid; IDA.
GO; GO:0005739; C:mitochondrial IDA.
GO; GO:0004855; F:wetol-acid reductoisomerase activity; TAS.
GO; GO:0009082; P:branched chain family amino acid biosynthesis; TAS.
GO; GO:000002; P:mitochondrial genome maintenance; IMP.
InterPro; IPR000506; AcH_isomrdctse.
PF01450; IlVC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                      Amino-acid biosynthesis; Branched-chain amino acid biosynthesis; Complete proteome; Direct protein sequencing; Magnesium; Mitochondrion; NADP; Oxidoreductase; Transit peptide.

TRANSIT 1 Mitochondrion (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.8%; Score 1503; DB 1; Length 395; 72.9%; Pred. No. 1.8e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ketol-acid reductoisomerase NADP (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Xie Q., Jimenez A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D76419A6AD68E85E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365 QPDYREKYEAEMEEIRNLEIWRAGKAVRSLRPENQ 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrophilic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44368 MW;
                                                                                                                                                                                                                                                                                                                                               TIGREAMS; TIGRO0465; ilvC; 1.
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nes 288; Conservative
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002341;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 AA;
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REGION
ACT SITE
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CHAIN
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Query Match
71.6%; Score 1499.5; DB 1; Length 404;
Best Local Similarity 71.1%; Pred. No. 3.3e-99;
Matches 286; Conservative 56; Mismatches 53; Indels 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                            WERADWPKEKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSWKDAVQD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYLYKTTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEATQSL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YPLIGANGMDWMYBACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQRSLDYNS 364
                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=2184401; PubMed=11859360; DOI=10.1038/nature724; Webline=2184401; PubMed=11859360; DOI=10.1038/nature724; Wood V., Gwilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A., Sgourcos J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S., Erooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E., J., Hunt S., Jagels K., James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
                                                                                                                                                                                                                                                                                                                                                                10 LRPMARQL---ATPAVQRRSFVAASSMVRATRKAA--VAPTQQQIRGVKTMDFAGHKEQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHGFSPVFKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIALGVAIGS
                                                                                   GO; GO:0004455; F:ketol-acid reductoisomerase activity; IEA. GO: 0009082; P:branched chain family amino acid biosynthesis; IEA
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       778827; 042619; 20. Created) 20. MAY-2000 (Rel. 39, Created) 20. MAY-2000 (Rel. 39, Created) 116-0CT-2001 (Rel. 40, Last sequence update) 113-SEP-2005 (Rel. 48, Last annotation update) Probable ketol-acid reductoisomerase, mitochondrial precursor EC 1.1.1.86) (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil reductoisomerase).
                                                                                                                                                                                                                                                                                               . 9
                                                                                                                                                                                                                                            71.7%; Score 1501; DB 2; Length 395; 72.9%; Pred. No. 2.5e-99; ive 44; Mismatches 57; Indels
                                                                                                                             InterPro; IPR000506; AcH isomrdctse.
Pfam; PF01450; IlvC; 1.
TIGRPAMs; TIGR00465; ilvC; 1.
SEQUENCE 395 AA; 44385 MW; DID319A6A238E85E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=i1v5; ORFNames=SPBCS6F2.12;
Schizosaccharomyces pombe (Fission yeast).
Elukaryota; Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaeses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPDYREKYEAEMEBIRNLEIWRAGKAVRSLRPENO 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         404 AA
                                       Ensembl; YLR355C; Saccharomyces cerevisiae.
SGD; S000004347; ILV5.
EMBL; S77496; AAB33579.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                 Best Local Similarity 72.9%
Matches 288; Conservative
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                   A Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B.,
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A Goffeau A., Cadieu E., Dreans S., Gloux S., Lehrach H., Reinhardt R.,
A Goffeau A., Cadieu E., Dreans S., Gloux S., Lelaure V., Mottier S.,
A Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
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Rybacovski G.V., Ussery D., Barrell B.G., Nurse P.,
The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP(+)
= (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
-!- CATALYTIC ACTIVITY: (2R,3R)-2,3-dihydroxy-3-methylpentanoate +
NADP(+) = (S)-2-hydroxy-2-ethyl-3-oxobutanoate + NADPH.
-!- PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-isoleucine from 2-oxobutanoate: step 2.
-!- PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H., "Identification of open reading frames in Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from pyruvate: step 2.
-!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
-!- SIMILARITY: Belongs to the ketol-acid reductoisomerase family.
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Probable ketol-acid reductoisomerase.
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Amino-acid biosynthesis; Branched-chain amino acid biosynthesis; Complete proteome; Mitochondrion; NADP; Oxidoreductase;
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Rutherford K.M., Rutter S., Saunders D., Seeger K.,
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InterPro; IPR000506; AcH_isomrdctse.
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EMBL; AB009603; BAA24000.1; -; mRNA.
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MEDLINE=98162722; PubMed=9501991;
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"Cloning and molecular analysis of two different ILV5 genes from a continuous strain of Saccharomyces cerevisiae.";

"Curr. Genet. 26:398-402(1994).

"EMBL; S77495; AAB33578.1; -; Genomic_DNA.

"R SSP, Q01222, 10WG.

"Ensembl; YLR355C; Saccharomyces cerevisiae.

"GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.

InterPro; IPR00506; AcH_isomractse.

"R TIGRFAMS; TIGR00465; ilvC; 1.

"TIGRFAMS; TIGR00465; ilvC; 1.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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MEDLINE=95179792; PubMed=7874731; DOI=10.1007/BF00309925;
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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

March 22, 2006, 15:21:27; Search time 123.747 Seconds (without alignments) 2252.046 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-797-248A-2 2071 1 MLRTQAARLICNSRVITAKR.....RNMEIWKVGKEVRKLRPENQ 395

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2166443 Total number of hits satisfying chosen parameters:

2166443 segs, 705528306 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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ALIGNMENTS

NUCLECTIDE SEQUENCE. RN WICLIMEPA117524; PubMed=3027658; RX WEDLIMEPA117524; PubMed=3027658; RX WEDLIMEPA117524; PubMed=3027658; RX "The ILVS gene of Saccharomyces cerevisiae is highly expressed."; RX Nucleic Acids Res. 14:9631-9651(1986). RX WICLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]. RX Nucleic Acids Res. 14:9631-9651(1986). RX GSTRAINS-2880c / AB972; RX MEDLIMES-97313267; PubMed=9169871; RX JOHNSTON M., Hillier L.W., Riles L., Albermann K., Andre B., RA Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., RA Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., RA Heumann K., Heuss-Neitzel D., Hilbert H., Obermaier B., Rieger M., RA Moestler P., Usernelle D., Purnelle B., Rechmann S., Rieger M., RA Pohl T.M., Portectalle D., Purnelle B., Rechmann S., Rieger M., RA Nehassel F., Vierendeels F., Voet M., Volckaert G., Voss H., RA Wenhassel F., Werendeels F., Voet M., Volckaert G., Voss H., RA Hani J., Hoheisel J.D., RA Hani J., Hoheisel J.D., RA Meuture 387:87-90(1997). RY The nucleotide sequence of Saccharomyces cerevisiae chromosome XII." RY MEDLINE-S202388; pubMed=7895733; RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., RA Verdens J.I., Putcher B., Kobayashi R., Latter G.I., Schwender B., RY Widebase "." RY Gatcher B., Robayashi R., Electrophoresis 15:1466-1486(1994). RY IDENTIFICATION OF PROBABLE N-TERMINUS.

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301 YPLIGKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFNS 360
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MEDLINE=55179792; PubMed=7874731; DOI=10.1007/BF00309925;

MEDLINE=55179792; PubMed=7874731; DOI=10.1007/BF00309925;

MEDLINE=55179792; PubMed=7874731; DOI=10.1007/BF00309925;

Lu Cloning and molecular analysis of two different ILV5 genes from a brewing strain of Saccharomyces cerevisiae.";

Lur. Genet. 26:398-402(1994).

REBL; 877496; AAB33579.1; -; Genomic_DNA.

RESSP; Q01292; 1QMG.

RESSP; Q01090455; F:Retol-acid reductoisomerase activity; IEA.

GO; GO:0009082; P:Dranched chain family amino acid biosynthesis; IEA.

RO; GO:0009082; P:Dranched chain family amino acid biosynthesis; IEA.

RIGREPMS; TIGROO465; 11VC; 1.

RIGREPMS; TIGRO0465; 11VC; 1.

SEQUENCE 395 AA; 44385 MW; D1D319A6A238E85E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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                                                                                                             361 QPDYREKLEKELDTIRNMEIWKVGKEVRKLRPENQ 395
                                                                          361 QPDYREKLEKELDTIRNMEIWKVGKEVRKLRPENQ 395
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                                                                                                                                                                                                                                                                                               395 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acetohydroxy-acid isomeroreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=ILV5; Synonyms=ILV5X;
                                                                                                                                                                                                                                                                                        Q02341 YEAST PRELIMINARY;
Q02341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.7
Matches 394; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B GO; GO:0042645; C:mitochondrial nucleoid; IDA.

R GO; GO:004455; C:mitochondrion; IDA.

R GO; GO:0004455; F:ketol-acid reductoisomerase activity; TAS.

R GO; GO:0009082; P:branched chain family amino acid biosynthesis; TAS.

R GO; GO:0000002; P:mitochondrial genome maintenance; IMP.

R D; Maino-acid biosynthesis; Ranched-chain amino acid biosynthesis;

R TIGREAMS; TIGRO0465; ilvC; I.

M Amino-acid biosynthesis; Branched-chain amino acid biosynthesis;

M Complete proteome; Direct protein sequencing; Magnesium;

Mitochondrion; NADP; Oxidoreductase; Transit peptide.

TRANSIT 1 Ketol-acid reductoisomerase.

T CHAIN 48 395 Ketol-acid reductoisomerase.

T NFEANSIT 1 
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Proc. Natl. Acad. Sci. U.S.A. 93:14440-14445(1996).

-!- CATALYTIC ACTIVITY: (R)-23-3dibydroxy-3-methylbutanoate + NADP(+)

= (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.

-!- CATALYTIC ACTIVITY: (2R,3R)-2,3-dihydroxy-3-methylpentanoate + NADPH.

NADP(+) = (S)-2-hydroxy-2-ethyl-3-oxobutanoate + NADPH.
                                                                                                                                                                                                                                                     isoleucine from 2-oxobutanoate: step 2.
PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLRIQAARLICNSRVITAKRIFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETV
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                                                                                                                                                                                    COFACTOR: Magnesium.
PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-
                                                                                                                                                                                                                                                                                                               from pyruvate: step 2.
SUBCELLULAR LOCATION: Mitochondrial.
SIMILARITY: Belongs to the ketol-acid reductoisomerase family.
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Ensembl; YLR355C; Saccharomyces cerevisiae.
SGD; S000004347; ILVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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Les 395; Conservative
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395
171
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HSSP; Q01292; 10MG.
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PubMed=15229592; DOI=10.1038/nature02579;

PubMed=15229592; DOI=10.1038/nature02579;

A Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontain I., Addle M., Anthouard V., Barbe C., Talla E., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C., Bastrame A., Boyer J., Cattolico L., Confanloleri F., de Daruvar A., Bospons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Nicaud J.-M., Nikolski M., Lesur I., Ma L., Muller H., Nicaud J.-M., Nikolski M., Lesur I., Ma L., Muller H., Swennen D., Tekaia F., Resolowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A., Zoudron B., Scarpelli C., Gaillardin C., Weissenbach J., Mincker P., Souciet J.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 TVETVYERADWPREKLLDYFKNDTFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWK 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 ATQSLYPLIGKYGMDYMYDACSTTARRGALDWYPIFKDALKPVFQDLYESTKNGSETKRS 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 VAVGSGYVYQTTFEKEVNSDLYGERGCLMGGIHGMFLAQYEVLRENGHSPSEAFNETVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MLRTQAARLICNSRVITAKRTFALATRAAAYSRPAA----RFVKPMITTRGLKQINFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 VFKDLTHVEPPKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 VAIGSGYVYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 ATQSLYPLIGKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; CR389948; CAGS8005.1; -; Genomic DNA.
GO; GO:0004455; F:ketol-acid reductoisomerase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0009082; F:branched chain family amino acid biosynthesis; IEA.
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06CY71 KLULA

10 QGCY71 KLULA PRELIMINARY; PRT; 397 AA.

AC 06CY71;

DT 25-OCT-2004 (TrENBLrel. 28, Last sequence update)

DF 25-OCT-2004 (TrENBLrel. 28, Last sequence update)

DF 1140 of Kluyveromyces lactis strain NRRL Y-1140 chromosome A of strain NRRL Y-1140 of Kluyveromyces lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.9%; Score 1903; DB 2; Length 399; 89.5%; Pred. No. 3e-129; ive 26; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399 AA; 44568 MW; E2241C86A034D728 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356 LEFNSQPDYREKLEKELDTIRNMEIWKVGKEVRKLRPENQ 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000506; AcH_isomrdctse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01450; IlvC; 1. TIGREAMS; TIGR00465; ilvC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 89.5% Matches 358; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 430:35-44(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. SEQUENCE 399 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YERADWPREKTLANYFKDDTFALIGYGSQGYGQGLAIRBNGLAVIIGVRKDGASWKAAIED 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 YERADWPREKLLDYFKNDTFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWKAAIED 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYVYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEATQSL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YPLIGKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFNS 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Curr. Genet. 26:398-402(1994).

EMBL; S77485; AAB33578.1; -; Genomic_DNA.

HSSP; O01292; 1QMG.

Ensembl; YIR355C; Saccharomyces cerevisiae.

GO; GO:0004455; F:ketol-acid reductoisomerase activity; IEA.

GO; GO:000982; P:branched chain family amino acid biosynthesis; IEA.

InterPro; IPR000505, AcH_isomrdctse.

Pfam; PF01450; IIVC; 1.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
candida glabrata strain CBS138 chromosome B complete sequence.
OrderediocusNames=CAGLOB030479;
Candida glabrata (Yeast) (Torulopsis glabrata)
Eukaryota; Fungi; Ascomyocas, Saccharomyocina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                            genes from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.7%; Score 2023; DB 2; Length 395;
larity 97.0%; Pred. No. 6.2e-138;
Conservative 9; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                              MEDLINE=95179792; PubMed=7874731; DOI=10.1007/BF00309925; Xie Q., Jimenez A.; "Cloning and molecular analysis of two different ILV5 gene brewing strain of Saccharomyces cerevisiae."; Curr. Genet. 26:398-402(1994).

EMBL: S77495; AAB33578.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMB; TIGR00465; ilvC; 1.
SEQUENCE 395 AA; 44309 MW; 2F8BCD94FD7E2AEF CRC64;
                                                                              01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QPDYREKLEKELDTIRNMEIWKVGKEVRKLRPENQ 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QPDYREKLEKELVTIRNMEIWKVGKEVRKLRPENK 395
  395 AA
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  PRT;
                                                     (TrEMBLrel. 01, Created)
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                                                                                                                              Acetohydroxy-acid isomeroreductase
Name=ILV5G;
002340_YEAST PRELIMINARY;
002340;
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                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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383; Conserv
                                                                                                                                                                                                                                                                  NCBI_TaxID=4932;
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05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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                                                                                                                                                                                                                                                                                                              STRAIN=ATCC 10895;
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SEQUENCE 394 AA;
                                                                                                                                                                                                                    NCBI_TaxID=33169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGD; ACL198W;
                                                                                      Name=ACL198W;
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                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;

Why wheels1222952; DOL=10.1038 / nature02579;

Dujou B., Sherman D., Fischer G., Durrens P., Casaregola S.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Lafontaine I., Aigle M., Anthouard V., Babour A., Barbe V.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Bospons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,

Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

A Rellanz S., Potler S., Richard G.-F., Straub M.-L., Suleau A.,

Seniou-Meyer M., Zivanovic Y., Bolotin-Pukuhara M., Thierry A.,

Mincker P., Souciet J.-L.;

Mincker P., Souciet J.-L.;

L Mature 430:35-44 (2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDGWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLIKGKTLYFSHGFSPVFK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLTHVEPPKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVAI 238
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GO; GO:0004455; F:ketcol-acid reductoisomerase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
InterPro; IPR000506; AcH_isomrdctse.
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                                         Aluyveromyces lacins (reast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7634BEC037ABAA9B CRC64;
                                                                                          Saccharomycetales; Saccharomycetaceae; Kluyveromyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSOPDYREKLEKELDTIRNMEIWKVGKEVRKLRPEN 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ą
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OrderedLocusNames=KLLA0A02673g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            397 AA; 44189 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01450; IlvC; 1. TIGREAMB; TIGR00465; ilvC; 1.
                                Kluyveromyces lactis (Yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 85.9
Matches 340; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
SEQUENCE 397 AA;
                                                                                                                       NCBI_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
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Q75CW4 AS:
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66 WPREKLLDYFKNDTFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWKAAIEDGWVPG 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVAIGSGYVYQ 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 PKDIDVILVAPKGSGRTVRSLFLEGRGINSSYAVWNDATGRAHEKAQALAVAVGSGYVYE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 TTFEKEVNSDLYGERGCLMGGIHGMFLAQYEVLRENGHSAFEAFNETGEEATQSLDPLIG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFNSQPDYR 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 WPREKLLEYFKNDTLALIGYGSQGHGQGLNLRDTGLKVVVGVRKGGASWKAAVEDGWVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTFEREVNSDLYGERGCLMGG1HGMFLAQYDVLRENGHSPSEAFNETVEEATQSLYPLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 AKRTFALATRAAAY-----SRPAARFVK-----PMITTRGLKQINFGGTVETVYERAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO:0004455; F:ketol-acid reductoisomerase activity; IEA.
GO:0016491; F:oxidoreductase activity; IEA.
GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S. Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S., Mort. C., Poehlmann R., Luedi P., Choi S., Wing R.A., Flavier A., Gaffney T.D., Philippsen P.; archaromyces cerevisiae genome as a tool for mapping the ancient Saccharomyces cerevisiae genome."; Science 304:304-307(2004).

EMBL, ABOLEGIG, AAS51030.1; -; Genomic_DNA.
                                                                                                                                                                                                                                Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.1%; Score 1680; DB 2; Length 394;
81.5%; Pred. No. 4.1e-113;
ive 32; Mismatches 28; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 AA; 43675 MW; 15A4E4FB942ACDA3 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1] "
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKLEKELDTIRNMEIWKVGKEVRKLRPEN 394
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Pfam; PF01450; IlvC; 1.
TIGRFAMs; TIGR00465; ilvC; 1.
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DT 10-MAY-2005 (TrEWBLrel. 30,

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TIGRFAMS; TIGR00465;
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Matches 317; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 IEDGWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGKTLYFSHGFSPVF 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDLTHVEPPKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDLTHVEPPSNIDVILAAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAEEKAIAMAIA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGSGYVYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEAT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 IGSGYVYKTTFEREVNSDLYGERGCLMGGIHGMFLAQYEVLRENGHTPSEAFNETVEEAT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OSLYPLIGKYGMDYMYDACSTTARRGALDWYPIFKNALKPVRODLYESTKNGTETKRSLE 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OSLYPLIGKYGMDYMYDACSTTARRGALDWYPRFKDALKPVFEELYESVKNGSETKRSLE 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 RTQAARL--ICNSRVITAKRTFAL---ATRAAAYSRPAARFVKPMITTRGLKQINFGGTV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                        Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S., Asagee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T., Davis R.W., Scherer S., Thorstenson G. Candida albicans.", "The diploid genome sequence of Candida albicans.",
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=SC5314;
Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.
Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
Jones T., Scherer S., Agabian N.;
"Annotation of the Genome of Candida albicans.";
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reducto-isomerase.
OrderedLocusNames=DEHA0F10483g;
Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
Eukaryota; Fungi; Ascomycota; Saccharomycetias; Saccharomycetas; Saccharomycetaceae; Debaryomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CAUTION: The sequence shown here is derived from an EMBLA/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AACQ01000112; EAK94923.1; -; Genomic_DNA.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to ca|CA1983|CaILVS Candida albicans CaILVS ketol-acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.5%; Score 1667; DB 2; Length 400; 79.1%; Pred. No. 3.6e-112;
   Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=237561;
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                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004)
                                                                                                                                                             PubMed=15123810; DOI=10.1073/pnas.0401648101;
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nes 315; Conservative
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GO: OC:0016853; Filaomerase activity; TBA.
GO: GO:0004455; Filetol-acid reductoisomerase activity; IBA.
GO: GO:0009082; Pilaomered chain family amino acid biosynthesis; IBA.
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TIGRFAMB; TIGRO465; IlvC; 1.
Complete Protecome; Isomerase.
SEQUENCE 399 AA; 44352 MW; 53D67F203BD09113 CRC64;
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Likely mitochondrial ketol-acid reductoisomerase.
Name-ILV5; ORFNames-CaOl9.88;
Candida albicans SC5314.
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SCALE GENOMIC DNA]
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
STRAIN-CLIB 122 / E 150;
PubMed=15229592; DOI=10.1038/nature02579;
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SEOUENCE 398 AA:
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                                                         STRAIN=SC5314;
PubMed=15123810; DOI=10.1073/pnas.0401648101;
PubMed=15123810; DOI=10.1073/pnas.0401648101;
Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
Davis R.W., Scherer S.;
"The diploid genome sequence of Candida albicans.";
Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=237561;
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                                                                                                                                                                    Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O. Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W., Jones T., Scherer S., Agabian N., annotation of the Genome of Candida albicans "; Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OrderedLocusNames=YALIOD011359;
Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Yarrowia lipolytica chromosome D of strain CLIB99 of Yarrowia
                                                                                                                                                                                                                                                                                                                                    80.3%; Score 1663; DB 2; Length 400; 78.9%; Pred. No. 7.1e-112; ive 42; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                             400 AA; 44882 MW; FC79162D05078D8C CRC64;
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EMBL; AACQ01000106; EAK95225.1; -; Genomic_DNA.
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Matches 314; Conservative
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QCAF8;
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Dujon B., Sheman D., Fischer G., Durrens P., Casaregola S.,
A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bospons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
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Wincker P., Souciet J.-L.;
I. "Genome evolution in yeasts.";
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GO; GO:0004455; F:ketol-acid reductoisomerase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
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Pfam; PF01450; IlvC; 1.
TIGRFAM8; TIGR00465; ilvC; 1.
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-I. CATALYTIC ACTIVITY: (2R. 3R) -2.3-dihydroxy-3-methylbutanoate + NADPH.

-I. CATALYTIC ACTIVITY: (2R. 3R) -2.3-dihydroxy-3-methylbentanoate + NADPH.

-I. CATALYTIC ACTIVITY: (2R. 3R) -2.3-dihydroxy-3-methylbentanoate + NADPH.
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PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine
                                                                                                                                                                                                   Sista H., Bowman B.;
Charactestrization of the ilv-2 gene from Neurospora crassa encoding
alpha-keto-beta-hydroxylacyl reductoisomerase.";
Gene 120:115-118(1992).
                                                                                                                                                       NUCLEOTIDE SEQUENCE.
MEDLINE-93013010; Pubmed=1398116; DOI=10.1016/0378-1119(92)90018-K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from pyruvate: step 2. SUBCELLUIAR LOCATION: Mitochondrial. SIMILARITY: Belongs to the ketol-acid reductoisomerase family.
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                                                                                                                                                                                                                                                                                                                                     STRAIN=74-0R23-1A / FGSC 987;
MEDLINE=22542210; PubMed=12655011; DOI=10.1093/nar/gkg293;
Mannhaupt G., Montrone C., Haase D., Mewes H.-W., Aign V.,
Hoheisel J.D., Fartmann B., Nyakatura G., Kempken F., Maier J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "What's in the genome of a filamentous fungus? Analysis of the Neurospora genome sequence.";
Nucleic Acids Res. 31:1944-1954(2003).
                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=74-OR23-1A / FGSC 987;
MEDLINE-22598136; PubMed=12712197; DOI=10.1038/nature01554;
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EMBL; AL670005; CAD21284.1; -; Genomīc DNA.
EMBL; AABX01000270; EAA32099.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                         Name=ilv-2; ORFNames=B11H24.150, NCU03608;
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Pfam; PF01450; IlvC; 1.
TIGRFAMB; TIGR00465; ilvC; 1.
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HSSP; Q9HVA2; INP3.
                                               Neurospora crassa.
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  reductoisomerase)
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Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
Burkhalt H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
A choepel Y., Callymore A., Cack P., Carw B., Dearellano K.,
Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
Brickson J., Faro S., Ferreira P., Fitzeerald M., Gage D., Galagan J.,
Gardyna S., Graham L., Grand-Pierre N., Hafez N.,
Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
Jaffe D., Johnson R., Jones C., Ramal M., Kamat A., Karetas A.,
Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
Mislsen C.B., Norbu C., O'Connell P., O'Neil D.,
Nielsen C.B., Norbu C., O'Connell P., O'Neil D.,
Aliesen C.B., Norbu C., O'Connell P., O'Donnell S.,
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                                                                                                                                                  Gaps
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                                                                                                             73.8%; Score 1528.5; DB 1; Length 402; 74.1%; Pred. No. 3.8e-102; tive 39; Mismatches 50; Indels 15;
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Glibberella zeae PH-1.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
     Ketol-acid reductoisomerase.
                                                                 Missing (in Ref. 1).
246F795898D2A174 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
11V5 NBUCK ketol-acid reductoisomerase, mitochondrial
acid reductoisomerase) (Alpha-keto-beta-hydroxylacil
                                                  T -> R (in Ref. 1).
Missing (in Ref. 1)
                    NADP (Potential).
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                                     Potential.
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                                                                                44623 MW;
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402 AA;
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                                                                                                           Query Match
Best Local Simi.
Matches 297;
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66 KEDVYERADMPQEKLLEYFKNDTLALIGYGSQGHGQGLALRDNGLAVIVGVRKNGKSWKD 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 LRGPARQLASAPRV--QRTFVSAARAAVRAGAVARPVASGPIQQQI--RGVKTMDFAGH
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Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P., Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S. Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M., Talamas J., Tesfaye S., Theodore J., Topham K., Travers M., Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B., Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                              "Fugarium graminearum genome sequence.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 405;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 72.8%; Score 1507.5; DB 2; Length Best Local Similarity 74.2%; Pred. No. 1.3e-100; Matches 296; Conservative 37; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405 AA; 44908 MW; 61C6AF99723A33FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFNSOPDYREKLEKELDTIRNMEIWKVGKEVRKLRPENQ 395
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AACM01000419; EAA67345.1; -; Genomic_DNA.
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Hypochetical protein.
ORFNames=MG01808.4;
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Q52F28;
                                                                                                                                                                                                                                                                                                                                                                                                       data.
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RA Borjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Frickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Frickschind M., Foldy K., Gage D., Galagan J., Gearin G., Gherre S.,
RA Girke A., Goyette A., Graham J., Grandbois E., Gyalten K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Hann T., Horn A., Houde N., Hughes L., Hulme W., Hubby E., Illev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamwysselis M., Karlsson E.,
RA Land D., Landers T., Leger T., Leger J., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokyiteang T., Lokyiteang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Mard K., Matches C., Maucell E.,
Mcarthy M., Mcdonough S., Mcghee T., Meldrin J., Mancell E.,
Mcarthy M., Mcdonough S., Mcghee T., Mikkelsen T., Mlenga V., Moru K.,
RA Maning J., Marballa R., Minova T., Mikkelsen T., Mlenga V., Moru K.,
RA Morathy M., O'donnell P., Okoawo O., O'leary S., Contosho B.,
Norbu N., O'donnell P., Okoawo O., O'leary S., Contosho B.,
Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Raymond C.,
RA Sheridan J., Sherpa N., Salmae-thomann N., Stavropoulos S.,
Ra Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
Ra Spencer B., Stalker J., Smirnov S., Smith C., Sougnez C.,
Ra Fetson K., Stone C., Stubbs M., Talamas J., Tchninga P.,
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Ramer A., Lander B., Stalker B., Ret E., Young G., Zainoun J., Zembeck L.,
Ramer A., Stook E., Wilkinson J., Wu Y., Wyman D., Zambeck L.,
Ramer A., Zody M., Lander E., Young G., Zainoun J., Zadav S.,
Ramer A., Zody M., Lander E., Young G., Zainoun J., Zadav S.,
Ray Sang S., Yene E., Young G., Zainou J., Young G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 WERADWPKEKLIEYFKDDTLALIGYGSQCHCQCINIRDNGLNVIIGVRKDGKSWKDAVQD 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.8%; Score 1507; DB 2; Length 4 Best Local Similarity 73.2%; Pred. No. 1.4e-100; Matches 289; Conservative 44; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=70-15;
Dean R., Mitchell T., Brown D., Pan H., Thon M.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The genome sequence of Magnaporthe grisea.";
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 400 AA; 44723 MW; 4C89B9E1495B6D75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary data.

EMBL, AACU01000121; EAAS6157.1; -; Genomic_DNA.
InterPro; IPR000506; AcH isomrdctse.
InterPro; IPR009014; Transketo_C_like.
Pfam; PF01450; IlvC; 1.
TIGRPAMS; TIGR00465; ilvC; 1.
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QAARLICNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETVYERA
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Best Local Similarity 71.1%
Matches 278; Conservative
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A Arroya J., Berriman M., Abderson M.J., Wortman J., Kim H.Stanley,

A Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,

Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,

Barman M., Fedorova N., Feldblyum T.V., Fischer R.,

Posker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,

Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,

Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,

Keller N., Khouri H., Kitamotto K., Kobayashi T., Kulkarni R.,

Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,

Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,

Mouyna I., Mulligan S., Miller B.L., Mohamoud Y., Molina M.,

Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,

Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,

Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,

Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,

Takeuchi M., Tekias F., Trurer G., Varquez de Adana C.R., Weidman J.,

White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,

Machida M., Hall N., Barrell B., Denning D.W.;

Machidia M., Hall N., Barrell B., Denning D.W.;

Macharia M., Machila M., Barrell B., Denning D.W.;

Macharia M., Machila M., Barrell B., Denning D.W.;
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               245 GYLYKTTFEKEVYSDLYGERGCLMGGIHGMPLAQYEVLRERGHSPSEAFNETVEEATJQSL 304
                                                            YPLIGKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFNS 360
                                                                             305 YPLIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQRSLDYNS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DWPREKLLDYFKNDTFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWKAAIEDGWVP 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                   Aspergillus fumigatus A£293.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             508 AA; 56353 MW; 09C99AB04D9D92EC CRC64;
                                                                                                                                                                                                                                                        13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                      365 QPDYREKYEAEMEEIRNLEIWRAGKAVRSLRPENQ 399
                                                                                                                      361 OPDYREKLEKELDTIRNMEIWKVGKEVRKLRPENQ 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary data.
EMBL; AAHF01000002; EAL92139.1; -; Genomic_DNA.
                                                                                                                                                                                                                                508 AA.
                                                                                                                                                                                                                                                                                                     Ketol-acid reductoisomerase.
ORFNames=Afu3g14490;
                                                                                                                                                                                                                              O4WYW4 ASPFU PRELIMINARY;
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nes 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus fumigatus.";
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                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=330879;
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Af293;
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Arachchi H.M., Barna N.; Bastien V., Bloom T., Boguslavkiy L.,
RA Arachchi H.M., Barna N.; Bastien V., Bloom T., Boguslavkiy L.,
RA Burkgalter B., Butler J., Calvo S.B., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cooke P., Cooke P., Dearellano K.,
RA Choepel Y., Collymore S., Perreira P., FitzGerald M., Gage D., Galagan J.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Gardyna D., Hagos B., Hall J., Horton L., Hulme W., Illav I.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Liu G., Lui A.,
Rells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
Ralls C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
Ralls C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
Ralls C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
A Miblova T., Menga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
A Nielsen C.B., Norbu C., O'Comor T., Oponnell P., O'Neil D.,
A Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
Rachupka A., Ramaeamy V., Mryphy T., Seaman S., Severy P., Smirnov S.,
Ramas J., Tesfave S., Schupback R., Seaman S., Severy P., Smirnov S.,
Ralamas J., Tesfave S., Theodore J., Topham K., Travers M.,
Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
Ralander E.,
                               297 VPKDVDVILVAPKGSGRTVRTLFREGRGINSSIAVYQDVTGKAKEKAIAMGVAVGSGYLY 356
                                                                                                                                                                                                                                                                                                                                                 GANGMDWMYAACSTTARRGAIDWSSRFKDTLKRPIENELYDSVRDGTETKRSLEYNSQKDY 476
                                                                                                                                                  304
                                                                                                                                                                                                                                                                                                     305 GKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFNSQPDY 364
                                                                                                                                                                                          PPKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVAIGSGYVY
                                                                                                                                              QTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEATQSLYPLI
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AACDO1000043; EAA64631.1; -; Genomic_DNA.
GO; GO:0004455; F:kecol-acid reductoisomerase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:000982; P:branched chain family amino acid biosynthesis; IEA.
InterPro; IPR00056; ACH_isomrdctse.
Pfam; PF01450; IlvC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400 AA; 44354 MW; F76A7F2A5AB65FA1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Fungi, Ascomycota, Pezizomyc
Eurotiales, Trichocomaceae, Emericella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSBAA4_EMENI PRELIMINARY;
QSBAA4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
ORFNames=AN2526.2;
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Gaps 2; 64

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DWPREKILDYFKNDTFALIGYGSQGYGQGLNIRDNGINVIIGVRKDGASWKAAIEDGWVP 124
                                GKNLFTVEDAIKRGSYVANILLSDAAQSETWPAIKPLITKGKTLYFSHGFSPVFKDLTHVE 184
                                                                    369 REKYEKEMQEIRDLEIWRAGKAVRSLRPENQ 399
                                                                                                          REKLEKELDTIRNMEIWKVGKEVRKLRPENQ 395
                                         129
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              65
                       69
                                 125
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Search completed: March 22, 2006, 15:33:25 Job time : 124.747 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

Title: Perfect score: Sequence:

US-10-797-248A-3
2086
1 MAARNCTKALRPLARQLATP.....IRNLEIWRAGKRSLRPENQK 400

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 2166443 seqs, 705528306 residues Searched:

2166443

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P38674 neurospora	8	-						Q59xr8 candida alb	Q6cy71 kluyveromyc			Q6fxg6 candida gla		Q02340 saccharomyc	Q75cw4 ashbya goss		Q5kfa0 cryptococcu				Q519j3 bacteroides	Q64ptl bacteroides	Q8a612 bacteroides	ın		w	aquifex a	Q8u2a3 pyrococcus	Oguz09 pyrococcus	
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SUMMARIES	ID	1LV5 NEUCR		Q4HY4	Q4WYW	Q5BAA.	Q6CAF		QS9WWS_CANAL				Q02341_YEAST				Q75CW4				Q4P572_USTMA				Q8A612					_	ILVC PYRAB	ILVC_LISIN
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	Length	402	400	405	208	400	398	399	400	400	397	395	395	399	404	395	394	401	401	401	625	352	362	347	359	344	341	341	333	332	332	331
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de	Query Match	99	83	87	78	77	74	73	73	73	73	72.	72.	71	71	70.	70.	68	89	89	53	22	22	22	21	2	5	24	23	23	23	23
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ILVC_LISMF	ILVC_LISMO	ILVC_METAC O65GI7 BACLD	ILVS PEA	ILVC_GLOVI 065XK0 ORYSA	ILVS ARATH	ILVC_CLOAB	Q5WEN2_BACSK
		7 7		1 11 12		-	7
331	331	335 342	581	332	335	337	341
23.2	23.0	22.5	22.5	22.5	22.3	22.2	22.2
484.5	480.5	470	469.5	469	465	463	463
32	34 35	36 37	8 6 6 6	4 4 0 1	4 4 3 E	44	45

ALIGNMENTS

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13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                            Hypothetical protein.
ORFNames=MG01808.4;
Magnaporthe grisea 70-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
                                                                                                                                    NUCLEOTIDE SEQUENCE.
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                                                                                                         NCBI_TaxID=242507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=70-15;
 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GHKEEVHERADWPAEKLLDYFKNDTLALIGYGSQGHGQGLNLRDNGLNVIVGVRKNGKSW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GHKEEVHERADWPAEKLLDYFKNDTLALIGYGSQGHQQGLNLRDNGLNVIVGVRKNGKSW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDAIQDGWVPGKNLFDVDEAISRGTIVMNLLSDAAQSETWPHIKPQITKGKTLYFSHGFS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 EATOSLYPLIGAHGMDWMFDACSTTARRGAIDWTPKFKDALKPVFNNLYDSVKNGDETKR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAARNCTKALRPLARQLATPAVQRRTFVAAASAVRASVAVKAVAAPARQQVRGVKTMDFA 60
                                                                      isoleucine from 2-oxobutanoate: step 2. PATHWAY: Amino-acid biosynthesis; L-valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 EDAIQDGWVPGKNLFDVDEAISRGTIVMNLLSDAAQSETWPHIKPQITKGKTLYFSHGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVFKDLTKVEVPTDVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEKAVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAARNCTKALRPLARQLATPAVQRRTFVAAASAVRASVAVKAVAAPARQQVRGVKTMDFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                         PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-
                                                                                                 from pyruvare: step 2.
SUBCELLULAR LOCATION: Mitochondrial.
SIMILARITY: Belongs to the ketol-acid reductoisomerase family.
 Amino-acid biosynthesis; Branched-chain amino acid biosynthesis; Magnesium; Mitochondrion; NADP; Oxidoreductase; Transit peptide.
TRANSIT 1 26 Mitochondrion (Potential).
CHAIN 20 99 NADP (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2069; DB 1; Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 3e-138;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 SLEYNSOPDYRERYEAELDEIRNLEIWRAGKAVRSLRPENOK 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential.
T -> R (in Ref. 1).
Missing (in Ref. 1).
246F795898D2A174 CRC64;
(S) -2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
                                                                                                                                                                                                                                                         EMBL; M84189; AAB00797.1; -; Genomic DNA.
EMBL; ALG70005; CAD21284.1; -; Genomic DNA.
EMBL; AC01000270; EAA32099.1; -; Genomic_DNA.
PIR; JC1428; JC1428.
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                                                                                                                                                                                                                                                                                                                                     InterPro, IPR000506; AcH_isomrdctse.
Pfam; PF01450; IlvC; 1.
TIGRPAMs; TIGR00465; ilvC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44623 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.2%;
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                                         COFACTOR: Magnesium.
                                                                                                                                                                                                                                                                                                                      HSSP; Q9HVA2; 1NP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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1D 05
AC 05:
DT 13
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RA BITTEN B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E., RAINH=70-15,

RA Arcachem H., Armbruster J., Barchantsang P., Baldwin J., Barry A.,

RA Arachem H., Armbruster J., Barchantsang P., Baldwin J., Barry A.,

RA Bayul T., Blitchastery B., Bloom T., Blye J., Boguslavskiy L.,

RA Galvos S., Camarata J., Campo K., Cooke P., Corum B., Cuomo C.,

RA Calvos S., Camarata J., Campo K., Cooke P., Corum B., Cuomo C.,

RA Calvos J., Camarata J., Campo K., Cooke P., Corum B., Cuomo C.,

RA Dorjee K., Dorris L., Duffer N., Doges A., Blkins T., Engels R.,

Brickson J., Farina A., Faro S., Ferreira P., Fischer H.,

R. Brickson J., Farina A., Faro S., Ferreira P., Fischer H.,

R. Brickson J., Raina B., Hall J., Hatcher B., Haller A., Haigdins H.,

R. Honan T., Horn A., Houde W., Hughes L., Hulme W., Hubby B., Iliev I.,

RA Jones C., Kamal M., Kamat A., Kamyysselis M., Karlsson E.,

R. Jones C., Kamal M., Kamat A., Kamyysselis M., Karlsson E.,

R. Jones C., Kamal M., Mcdonald J., Molean C., Major J.,

R. Muchail R., Marabella R., Maruk K., Macdonald J., Maclean C., Major J.,

R. Moszuthy M., Mcdonough S., Mcdhes T., Malursan S.,

R. Moszuthy M., Mcdonough S., Mcdhes T., Meldrim J., Menson G.,

R. Morell S., Rochupka T., Ramesan W., Maldrim J., Menson C.,

R. Morell S., Rachupka T., Ramesan W., Rogers U., Rogers C.,

R. Worbu N., O'donnell P., Okoawo O., O'leary S., Conctosho B., Patker S., Perrin D., Phunkhang P., Piqani B.,

R. Wetter R., Richardson S., Rise C., Rottiguez J., Rogers T.,

R. Sherpa N., Sherpa N., Shi J., Smirnov S., Smith C., Sougnes C.,

R. Sherpan M., Sherpa N., Shi J., Smirnov S., Smith C., Sougnes C.,

R. Sherson J., Whitaker C., Wilkinson J., Wade S., Wang S., Wang S., Tsamla T., Tsomo N., Vallee D., Vassillev Y., Topham K.,

R. Towey S., Tsamla T., Tsomo N., Vallee D., Vassillev Y., Topham K.,

R. Towey S., Tsamla T., Tsomo N., Vallee D., Wassillev Y., Waynon C.,

R. Wang S., Yang X., Yeager S., Weng S., Wang S., Wan
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                                                                                                                                                                                                                          Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
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Zhu H., Blackmon B.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The genome sequence of Magnaporthe grisea."; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dean R., Mitchell T., Brown D., Pan H., Thon M.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases
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Last sequence update)
Last annotation update)
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EMBL; AACU01000121; EAA56157.1; -; Genomic_DNA.

InterPro; IPR00506; AcH_isomrdctse.

InterPro; IPR009014; Transketo_C_like.
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TIGREAMS; TIGR00465; ilvC; 1.
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                                                                                                                                                                                           GHKEEVHERADWPAEKLLDYFKNDTLALIGYGSQGHGQGLNIRDNGLNVIVGVRKNGKSW 120
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                                                                                                                                                                                                                          BDAIQDGWVPGKNLFDVDEAISRGTIVMNLLSDAAQSETWPHIKPQITKGKTLYFSHGFS
                                                                                     1 MAARNCTKALRPLARQLATPAVQRRTFVAAASAVRASVAVKAVAAPARQQVRGVKTMDFA
                                                                                                                         PVFKDLTKVEVPTDVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEKAVAL
                                         Gaps
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
11VS NEUCR Ketol-acid reductoisomerase, mitochondrial (Acetohydroxy-acid reductoisomerase, Mathanacid reductoisomerase)
                                         4 ;
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Eukaryota; Pungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
NCBI_TaxID=229533;
                                   Indels
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             1.9e-123;
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87.1%; Preu. xx.
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Q4HY40;
                                   Conservative
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        Best Local Similarity
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Microman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
M. Microman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
M. Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,
M. Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
Roldman G.H., Gomi K., Griffith. Jones S., Gwilliam R., Haas B.,
A Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molliam M., Monod M.,
Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAARNCTKALRPLARQLAT-PAVQRRTFVAAA-SAVRASVAVKAVAA-PARQQVRGVKTM
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                      -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                      2; Length 405;
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                  87.2%; Score 1819.5; DB 2 86.4%; Pred. No. 1.5e-120;
                                                                                                                                           EMBL; AACM01000419; EAA67345.1; -; Genomic_DNA
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Q4wyw4;
                                                                                                                preliminary data.
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Matches 350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGFSPVFKDLTKVEVPTDVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVALGVAVGSGYLYETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFN 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETVERATOSLYPLIGAHGMDWMFDACSTTARRGAIDWTPKFKDALKPVFNNLYDSVRNGD 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J., White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K., Machida M., Hall N., Barrell B., Denning D.W.; "Genomic sequence of the pathogenic and allergenic filamentous fungus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S., Arachin H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L., Boukhgalter B., Butler J., Calvos S.E., Camarata J., Chang J., Chopel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K., Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R., Erickson J., Faro S., Ferreira P., Fitzderald M., Gage D., Galagan J., Gardyna S., Gnerre S., Grand-Pierre N., Hafez N., Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I., Hagopian D., Landers T., Lovine R., Lindblad-Toh K., Liu G., Lui A., Karates A., Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
                                                                                                                                                                                                                                                                                                                                                                            1 MAARNCTKALRPLARQLATPAVORRTFVAAA----SAVRASVAVKAVAAPARQQVRGVKT
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                   Aspergillus fumigatus.";
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION; The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                      16;
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Bukaryota; Fungl; Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                           Length 508;
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                                                                                                                                                                                                                                             508 AA; 56353 MW; 09C99AB04D9D92EC CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                         78.6%; Score 1639; DB 2; 78.8%; Pred. No. 1.2e-107; iive 35; Mismatches 35;
                                                                                                                                                                                                  EMBL; AAHF01000002; EAL92139.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-2005 (TrEMBLrel. 30,
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Matches 320, Conservative
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QSBAA4;
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Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
Nielsen C.B., Norbu C., O'Connor T., O'Donnell B., O'Neil D.,
Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Suubbs M.,
Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
                                                                                                                                                                                                                                                                                                                                                                                         "Genome Sequence of Aspergillus nidulans.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AACD01000043; EAA64631.1; -; Genomic_DNA.
GO; GO:0004455; F:ketol-acid reductoisomerase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
InterPro; IPR00506; ACH_isomrdctse.
TIGRFAMS; TIGR00465; ilvc; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GHKEEVHERADWPAEKLLDYFKNDTLALIGYGSQGHGQGLNLRDNGLNVIVGVRKNGKSW
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OrderedLocusNames=YALIOD03135g;
Varrowia lipolytica (Candida lipolytica)
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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Last annotation update)
ome D of strain CLIB99 of Yarrowia
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400 AA; 44354 MW; F76A7F2A5AB65FA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 77.2%; Score 1611; DB 2; Local Similarity 78.1%; Pred. No. 8.6e-106; nes 314; Conservative 36; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
STRAIN=CLIB 122 / E 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398 AA
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QCAR8;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last seq. 25-OCT-2004 (TrEMBLrel. 28, Last ann
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         Dujon B., Sharman D., Fischer G., Durrens P., Casaregola S.,
Lafoncaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
Goffard N., Prangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Robre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Janniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Muller H.,
Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic Y., Bolotin-Pukuhara M., Thierry A.,
Bouchler C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
"Genome evolution in yeasts.",
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GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
InterPro: IPR000506; ACH isomrdctse.
Pfam; PF01450; IIVC; 1.
TIGRFAMS; TIGR00465; ilvC; 1.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces
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06BL24_20CT-2004 (TrEWBLrel. 28, Created)
25-OCT-2004 (TrEWBLrel. 28, Last sequence update)
25-OCT-2004 (TrEWBLrel. 28, Last sequence update)
Similar to ca|CA1983|CaILV5 Candida albicans CaILV5 ketol-acid
                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 398;
                                                                                                                                                                                                         Nature 430:35-44(2004).
EMBL; CR382130; CAG80542.1; -; Genomic_DNA.
GO; GO:0004455; F:ketol-acid reductoisomerase activity; IEA.
                                                                                                                                                                                                                                                                                                                                          74.8%; Score 1560.5; DB 2; Leuyl...
75.1%; Pred. No. 3.2e-102;
Migmatches 52; Indels
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PubMed=15229592; DOI=10.1038/nature02579;
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                                                                                                                                                                                                                                                                                                                             44160 MW;
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Matches 301; Conservative
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CSTRAIN-ATCC 36239 / CBS 767;

PubMed=15229592; DOI=10.1038/nature02579;

PubMed=15229592; DOI=10.1038/nature02579;

PupOn B., Sherman D., Fischer G., Durrens P., Casaregola S.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Boistame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

Bospons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,

Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

Nicaud J.-M., Nikolski M., Oztar S., Oztar-Kalogeropulos O.,

Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,

Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,

Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,

Mincker P., Souici J.-L.,
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GO; OG:0016853; Filsomerase activity; IEA.
GO; GO:0004455; Filsetol-acid reductoisomerase activity; IEA.
GO; GO:0009082; Pilsetol-acid reductoisomerase activity; IEA.
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Likely mitochondrial ketol-acid reductoisomerase.
Name=ILV5; ORFNames=CaO19.7733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.9%; Score 1542; DB 2; 72.9%; Pred. No. 6.6e-101; ive 49; Mismatches 54;
SEQUENCE [LARGE SCALE GENOMIC DNA]
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Complete proteome; Isomerase.
SEQUENCE 399 AA; 44352 MW;
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Matches 293; Conservative
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Q59WWS;
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NCBI_TaxID=237561;
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                                                                                                                                                                                                                                      STRAIN=SC5314;
PubMed=15123810; DOI=10.1073/pnas.0401648101;
PubMed=15123810; DOI=10.1073/pnas.0401648101;
Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
Davis R.W., Scherer S.;
"The diploid genome sequence of Candida albicans.";
Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
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                                    Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, mitosporic Saccharomycetales, Candida
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059XR8;
059XR8;
10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
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114kely mitochondrial ketol-acid reductoisomerase.
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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                                                                                                                   NCBI_TaxID=237561;
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                                                                                                                                                                                                                                                                                                                      Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O., Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W., Jones T., Scherer S., Agabian N.;

"Annotation of the Genome of Candida albicans.";

"Annotation of the Genome of Candida albicans.";

Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

-!-CANTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AACQ01000106; EAK95225.1; -; Genomic_DNA.
                                                  PubMed=15123810; DOI=10.1073/pnas.0401648101;
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Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
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Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetaceae, Kluyveromyces.

NCBI_TaxID=28985;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Kluyveromyces lactis strain NRRL Y-1140 chromosome A of
1140 of Kluyveromyces lactis.
OrderedLocusNames=KLLA0025739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERKRSLEYNSQPDYRERYEAELDEIRNLEIWRAGK--RSLRPENQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.6%; Score 1535.5; DB 2
72.8%; Pred. No. 1.9e-100;
:ive 47; Mismatches 52;
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Q6CY71;
SEQUENCE
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Saccharomyces cerevisiae (Baker's yeast).
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;

Why Medial 5225952; DOI=10.1038/nature02579;

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Wincher D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 HERADWPAEKLLDYFKNDTLALIGYGSQGHGQGLNLRDNGLNVIVGVRKNGKSWEDAIQD 126
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GO; GO:0004455; F:ketol-acid reductoisomerase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
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01-JAN-1988 (Rel. 06, Last sequence update)
113-SEP-2005 (Rel. 48, Last annotation update)
Ketol-acid reductoisomerase, mitochondrial precursor (EC 1.1.1.86)
(Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil reductoisomerase).
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"Genome evolution in yeasts.";
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MEDLINE=97313.67; PubMed=9169871;
A Johnston M., Hillier L.W., Riles L., Albermann K., Andre B.,
Ansorge W., Benes V., Euckner M., Delius H., Dubois E.,
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Hani J., Hoheisel J.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ween the Swiss Institute of Bioinformatics and the EMBL outstation
European Bioinformatics Institute. There are no restrictions on it
as long as its content is in no way modified and this statement is no
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-! CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADPH.
-! CATALYTIC ACTIVITY: (R)-3,3-dihydroxy-3-methylpentanoate + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-isoleucine from 2-oxobutanoate: step 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from pyruvate: step 2.
-!- SUBCELLULAR LOCATION: Mitochondrial.
-!- SIMILARITY: Belongs to the ketol-acid reductoisomerase family.
                                                                                                                                                                       "The ILVS gene of Saccharomyces cerevisiae is highly expressed."; Nucleic Acids Res. 14:9631-9651(1986).
                        Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender F
Volpe T., Warner J.R.; McLaughlin C.S.;
"Protein identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                                                                                [2]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=S288c / AB972;
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GO; GO:0042645; C:mitochondrial nucleoid; IDA.
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SWISS-2DPAGE, POG168, YEAST.
Ensembl; YLR355C; Saccharomyces cerevisiae.
SGD, SOG0004347, ILVS.
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EMBL; U19102; AAB67753.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Electrophoresis 15:1466-1486(1994).
                                                                                                                           MEDLINE=87117524; PubMed=3027658; Petersen J.G.L., Holmberg S.; "The ILVS gene of Saccharomyces o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95203288; PubMed=7895733;
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                                                                                         [1]
NUCLEOTIDE SEQUENCE.
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ALL STATES

Name=ILV5; OrderedLocusNames=YLR355C; ORFNames=L9638.7;

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S000004347; ILV5
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R GO; GO:0005739; C:mitochondrion; IDA.

R GO; GO:000455; F:ketol-acid reductoisomerase activity; TAS.

GO; GO:0000082; P:branched chain family amino acid biosynthesis; TAS.

R GO; GO:0000002; P:mitochondrial genome maintenance; IMP.

InterPro; IPR00105; AcH isomrdctse.

R Pfam; PF01456; IlvC; 1.

R TIGRFAMS; TIGR00465; ilvC; 1.

Amino-acid biosynthesis; Branched-chain amino acid biosynthesis;

Complete proteome; Direct protein sequencing; Magnesium;

Mitochondrion; NADP; Oxidoreductase; Transit peptide.

TRANSIT 1 47 Mitochondrion (Potential).

TRANSIT 1 48 395 Mitochondrion (Potential).

TRANSIT 1 48 395 Mitochondrion) (Potential).
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Cloning and molecular analysis of two different ILV5 genes from a brewing strain of Saccharomyces cerevisiae.";
Cur. Genet. 26:398-402(1994).
Embl. 577466; Aba33579.1; -; Genomic_DNA.
HSSP; Q01292; 1QMG.
Ensembl; YLR355C; Saccharomyces cerevisiae.
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Saccharomycetales, Saccharomycetaceae, Saccharomyces,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                        72.3%; Score 1508.5; DB 1; Length 395; 73.6%; Pred. No. 1.6e-98; tive 39; Mismatches 50; Indels 17;
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MEDLINE=95179792; Pubmed=7874731; DOI=10.1007/BF00309925;
                                                                                                                                                                                                                                                                                    48 395 Ketol-acid reductoisomerae
84 93 NADP (Potential).
363 395 Hydrophilic.
171 Potential.
395 AA; 44368 MW, D76419A6AD68B85E CRC64;
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Last annotation update)
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Q02341 YEAST
QC2341 YEAST
AC QC2341,
DT 01-NOV-1996 (TYEMBLEEL. 01,
DX NCEL-TOWN CECRETORY
COX SACCHATOMY CECRETORY
COX NCBL TAXID=4932;
RN (1) TAXID=4932;
RN MEDLINE=95179792; PubMed=787
RA Xie 0, Jimenez A.;
TCLONING and molecullar analy
RT TCLONING and molecullar analy
RT TCLONING and molecullar analy
RT CURT. Genet. 26:398-402(1994)
DR EMBL; 877496; AAB33579:1; -;
DR EMBL; 877496; AAB33579:1; -;
DR ENSEP; QO1292; LQMG.
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Best Local Simil
Matches 295; (
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TOTAL STRAIN-ATCC 2001 / CBS 2001 E., Talla E., A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E., A GOTTAN S., Blanchin S., Beckerich J.-M., Beyne E., Blabykasten C., Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Blaykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Boisrame A., Roszul R., Lemaire M., Lesur I., Ma L., Muller H., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nerlad J.-M., Nikolski M., Oztas S., Ozter-Kalogeropoulos O., Nellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A., Zhvanovin Y., Wesolowski-Louvel M., Westhof E., Wirth B., Zunanovin Y., Sulvar M., Thierry A., Zhvanovin Y., Bolotin-Fukuhara M., Thierry A., Wincker P., Souciet J.-L., Sarpelli C., Gaillardin C., Weissenbach J.,
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GO; GO:0004055; F:ketol-acid reductoisomerase activity; IEA.
GO; GO:0009082; F:ketol-acid reductoisomerase activity; IEA.
InterPro; IPR000066; ACH isomrdctse.
Pfam; PF01450; IlvC; 1.
TIGRPAMS; TIGR00465; ilvC; 1.
SEQUENCE 395 AA; 44385 MW; D1D319A6A238E85E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 PVPKDLTKVEVPTDVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEKAVAL
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Candida glabrata strain CBS138 chromosome B complete sequence.
OrderediocusNames=CAG10B030479;
Candida glabrata (Yeast) (Torulopsis glabrata).
Bukaryota, Pungi, Ascomycota, Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                     DB 2; Length 395;
                                                                                                                                                                                                                                                                                 Query Match 72.2%; Score 1506.5; DB 2; Length Best Local Similarity 73.6%; Pred. No. 2.2e-98; Matches 295; Conservative 38; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 SLEYNSQPDYRERYEAELDEIRNLEIWRAGK--RSLRPENQ 399
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Q6FXG6;
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AARNCTKALRPL-ARQLATPAVQRRTFVAAASAVRASVAVKAVAAPARQ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 DYMYDACSTTARRGALDWYPIFKDALKPVFQDLYESTKNGSETKRSLEFNSQPDYREKLE 373
                                                                                                                                                                                                    Wood V., Gwilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A., Sgouros J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G., Holroby S., Hornsby T., Howarth S., Huckle B.J., Hunk S., Jagels K., James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch B.,
                                                                                                                                                                                                                                                    KLLNYFANDTFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWKAAIEDGWVPGENLF
                                                                                                                                                                                     24 RRTFVAAASA-----VRASVAVKAVAAPARQQVRGVKTMDFAGHKEEVHERADWPAE
       EMBL, CR380948; CAG58005.1; -; Genomic DNA.
GO; GO:0004455; F:ketol-acid reductoisomerase activity; IEA.
GO; GO:0006491; F:oxidoreductase activity; IEA.
GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
InterPro; IPR000506; AcH isomrdctse.
Pfam; PF01450; IIvC; 1.
TIGRFAMB; TIGR00465; ilvC; 1.
                                                                                                                                                                Gaps
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                                                                                                                                                               15;
                                                                                                                                     DB 2; Length 399;
                                                                                                                                  71.9%; Score 1500.5; DB 2; Length 74.1%; Pred. No. 5.8e-98; ive 40; Mismatches 45; Indels
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MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
                                                                                                            E2241C86A034D728 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                                                                                            399 AA; 44568 MW;
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 Nature 430:35-44(2004)
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SEQUENCE 399 AA
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Wartren T., Whitchead S.,
Woodward J.R., Volckaert G., Aert R., Schaefer M., Mueller-Auer S.,
Ameltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Ameltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Ameltjens I., Vanstreels E., Rieger M., Fritzc C., Holzer E., Meestl D.,
Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
Pohl T.M., Eger P., Zimmermann W., Wedder H., Wambutt R., Purnelle B.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
Andlbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Ancas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Dominguez A., Revuelta J.L., Moreno S., Armetrong J., Forsburg S.L.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98162722; PubMed-9501991;
Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
"Identification of open reading frames in Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from pyruvate: step 2.
-!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
-!- SIMILARITY: Belongs to the ketol-acid reductolsomerase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probable ketol-acid reductoisomerase
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Complete proteome; Mitochondrion; NADP; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S -> R (in Ref. 2).
Y -> S (in Ref. 2).
N -> P (in Ref. 2).
N -> P (in Ref. 2).
V -> G (in Ref. 2).
W, 9AB3674C71AD6FEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL023288; CAA18891.1; -; Genomic_DNA.
EMBL; D89175; BAA13837.1; -; mRNA.
EMBL, AB006603; BAA24000.1; -; mRNA.
PIR; T40522; T40532.
HSSP; Q9HVA2; 1NP3.
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InterPro; IPR000506; AcH isomrdctse.
Pfam; PF01450; IlvC; 1.
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ilvC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 4:363-369(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 415:871-880(2002)
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71.6%; Score 1494.5; DB 1; Length 404; 69.7%; Pred. No. 1.6e-97; ive 52; Mismatches 46; Indels 27;

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230
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                                                                                         VGVRKNGKSWEDAIQDGWVPGKNLFDVDEAISRGTIVMNLLSDAAQSETWPHIKPQITKG 170
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                                                                                                                                                                                                                                               PSEAFNETVEEATQSLYPLIGAHGMDWMFDACSTTARRGAIDWTPKFKDALKPVFNNLYD 350
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                                      VRGVKTMDFAGHKEEVHERADWPAEKLLDYFKNDTLALIGYGSQGHGQGLNLRDNGLNVI 110
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                                                                                                                                                         SSRMAMKALRIMGSRRLATRSM-----SVMARTIAAPSMRFAPRMTAPLMQ
                                                     GKAKEKAVALGVAVGSGYLYETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTLYFSHGFSPVFKDLTKVEVPTDVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WUCLEOTIDE SEQUENCE.
MEDLINE=95179792; PubMed=7874731; DOI=10.1007/BF00309925;
Xie Q., Jimenez A.;
Xie Q., Jimenez A.;
Cloning and molecular analysis of two different ILV5 genes from a brewing strain of Saccharomyces cerevisiae.";
Curr. Genet. 26.398-402(1994).
EMBL; S77495; AAB33578.1; -; Genomic_DNA.
EMBL; S77495; Racharomyces cerevisiae.
GQ: GG:000455; F:ketol-acid reductoisomerase activity; IEA.
GQ: GG:0009082; P:branched chain family amino acid biosynthesis; IEA.
InterPro; IPR000506; AcH_isomrdctse.
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                                                                                                                                                                                                                                                                                                              Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetaceae, Saccharomyces.
NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                 351 SVKNGDERKRSLEYNSOPDYRERYEAELDEIRNLEIWRAGK--RSLRPENOK
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SEQUENCE 395 AA; 44309 MW; 2F8BCD94FD7E2AEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.9%; Score 1479.5; DB 72.2%; Pred. No. 1.8e-96; ive 43; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                         395 AA
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                                                                                                                                                                                                                                                                                                                                                                                         Q02340 YEAST PRELIMINARY;
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Matches 288; Conservative
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                                                                                              TQSLYPLIGAHGMDWMFDACSTTARRGAIDWTPKFKDALKPVFNNLYDSVKNGDERKRSL
                                              AVGSGYLYETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEA
                                                                                                                                           363 EYNSOPDYRERYEAELDEIRNLEIWRAGK--RSLRPENG 399
                                                                                                                                                          Search completed: March 22, 2006, 15:33:26 Job time : 126.313 secs
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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

March 22, 2006, 15:21:02 ; Search time 114.954 Seconds (without alignments) 1528.885 Million cell updates/sec

US-10-797-248A-3

Title: Perfect score:

1 MAARNCTKALRPLARQLATP.....IRNLEIWRAGKRSLRPENQK 400 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

2443163 seqs, 439378781 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

2443163

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2005s:* geneseqp1980s:* A_Geneseq_21:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Abr64305 Acetohydr	Abr64306 Acetohydr		Ą		Abi26477 Aspergill			Abj25877 Aspergill			Acetohyd	Adk64188 Disease t	Adb70124 C. neofor	Abu20976 Protein e	Aab96356 Putative	Aay26182 Soybean a		Ë			Corn	1 Plant	9 Plant
SUMMARIES	TD 01	ABR64305	ABR64306	ADV16807	ABR64303	ADV16810	ABJ26477	ABJ26502	ABJ25902	ABJ25877	AAU15089	ABP73238	ABR64304	ADK64188	ADB70124	ABU20976	AAB96356	AAY26182	AAU01250	ABB48168	ABU32456	AAY26183	AAY26180	ADX93651	ADX88429
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	Length	400	400	400	402	403	396	. 508	388	200	400	400	395	395	409	347	332	586	342	331	331	579	579	585	286
de	Query Match	100.0	89.2	89.2	89.0	79.5	78.3	78.3	76.9	76.9	73.8	73.8	72.3	72.3	68.2	52.0	23.3	23.3	23.2	23.0	23.0	22.7	22.7	22.7	22.7
	Score	2086	1860	1860	1856	1658	1633	1633	1604	1604	1539.5	1539.5	1508.5	1508.5	1423.5	1084.5	486	486	483	480.5	480.5	473	473	473	473
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ADY07198	ADY07344	ADX77584	ADM26226	AAG35210	AAG35209	ADY61069	AAG26356	ABB92723	ADT55519	ABU24174	ADY04361	ADY07450	ADX92449	ADY07435	AAG81458	ABU42920	ABP39068	ADS07053	ABU18526	AAG26357
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8	N	7	7	7	7	~	6	6	ď	'n	ö	8	6	8	~	~	ö	7	7	7
473	473	473	472.5	472	472	467	465	465	465	463	463	462	462	462	461.5	461.5	461.5	461.5	454.5	453.5
25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase. Morin V; Effantin G, ABR64305 standard; protein; 400 AA. Acetohydroxyacid isomeroreductase. Zundel JL, (AVET) AVENTIS CROPSCIENCE SA. 10-SEP-2001; 2001FR-00011689. 10-SEP-2001; 2001FR-00011689. 16-SEP-2003 (first entry) Lebrun MH, Neurospora crassa. FR2829363-A1. 14-MAR-2003. ABR64305; Dumas R) ABR64305

Treatment of crops, useful for controlling fungi on, e.g. cereals, potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid isomeroreductase. WPI; 2003-405775/39.

Claim 2; Fig 1; 66pp; French.

The present invention relates to a method for controlling fungal disease in crops by applying an inhibitor (I) of acetohydroxyacid isomeroreductase. (I) are used for curative or preventative treatment of a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or rape. The present sequence is an acetohydroxyacid isomeroreductase, used to illustrate the invention

Sequence 400 AA;

Gaps ö Length 400; Indels Query Match 100.0%; Score 2086; DB 6; Best Local Similarity 100.0%; Pred. No. 2.1e-191; Matches 400; Conservative 0; Mismatches 0;

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Gaps 4;

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Query Match
Best Local Similarity 87.1%;
Matches 350; Conservative 34
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                                                              GHKEEVHERADWPAEKLLDYFKNDTLALIGYGSQGHGQGLNLRDNGLNVIVGVRKNGKSW 120
                                                                                                                                                                                                GVAVGSGYLYETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVE 300
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of acetohydroxy acid
                                                GHKEEVHERADWPAEKLLDYFKNDTLALIGYGSQGHGQGLNLRDNGLNVIVGVRKNGKSW 120
                        9
              EDAIQDGWVPGKNLFDVDEAISRGTIVMNLLSDAAQSETWPHIKPQITKGKTLYFSHGFS
                                                                                                                                                                                                               GVAVGSGYLYETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antifungal; fungal disease; acetohydroxyacid isomeroreductase.
                                                                                               EDAIQDGWVPGKNLFDVDEAISRGTIVMNLLSDAAQSETWPHIKPQITKGKTLYFSHGFS
                                                                                                                                              PVFKDLTKVEVPTDVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEKAVAL
                                                                                                                                                               PVFKDLTKVEVPTDVDVILVAPKGSGRTVRSLFREGRGINSSPAVYQDVTGKAKEKAVAL
                                                                                                                                                                                                                                              EATQSLYPLIGAHGMDWMFDACSTTARRGAIDWTPKFKDALKPVFNNLYDSVKNGDERKR
MAARNCTKALRPLARQLATPAVQRRTFVAAASAVRASVAVKAVAAPARQQVRGVKTMDFA
                                                                                                                                                                                                                                                                                             SLEYNSQPDYRERYEAELDEIRNLEIWRAGKRSLRPENOK 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AVET ) AVENTIS CROPSCIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-405775/39.
N-PSDB; ACC80185, ACC80186.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lebrun MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Magnaporthe grisea
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illustrate the invention

Sequence 400 AA;

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                                                                                                                                                       59 GHKEQVWERADWPKEKLLEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSW
                                                                                         181 PVFKDLTKVEVPTDVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEKAVAL
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                                                                       1 MAARNCTKALRPLARQLATPAVQRRTFVAAASAVRASVAVKAVAAPARQQVRGVKTMDFA
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NV, Darveaux BA, Frank SA, Heiniger
Covington AS, Tarpey R, Shuster JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLEYNSOPDYRERYEAELDEIRNLEIWRAGK--RSLRPENOK 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          400
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, rred. No. 1.2e-169;
34; Mismatches 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      substrate inhibition; antibiotic; gene disruption;
ketol-acid reductoisomerase; ILVS; enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADV16807 standard; protein; 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAY-2003; 2003US-0470947P.
19-MAY-2003; 2003US-0471615P.
21-MAY-2003; 2003US-0472242P.
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N-PSDB; ADV16805, ADV16806.
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Montenegro-Chamorro MV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with a test compound
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The invention describes a method of identifying a test compound as a candidate for an antibiotic comprising contacting ornithine candidate for an antibiotic comprising contacting ornithine carbamoytransferase (Ocrase) or ketol-acid reductoisomerase polypeptide, or fungal pathogenicity-conferring gene with a test compound. The method comprises: contacting Ocrase polypeptide, ketol-acid reductoisomerase polypeptide or fungal pathogenicity-conferring gene with a test compound; and detecting the presence or absence of binding between the test compound and the polypeptide or gene, where binding indicates that the test compound and the polypeptide or gene, where binding indicates that the test compound at least 50% sequence denciding a solated nucleic acid comprising a nucleotide sequence encoding a losypeptide having at least 50% sequence identity to, or having at least 10% of the activity of, 400, 403 or 469 amino acids; and an isolated polypeptide consisting essentially of the amino acid sequence of 400, or 469 amino acids actide acids. The methods are useful for identifying inhibitors of or 469 amino acids. The action acids conferring gene as antibiotics. This is the amino acid curgal pathogenicity-conferring gene as antibiotics. This is the amino acid sequence of Magnaporthe grisea ketol-acid reductoisomerase ILV5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHKEEVHERADWPAEKLLDYFKNDTLALIGYGSQGHGQGLNLRDNGLNVIVGVRKNGKSW 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58
                                                                                                                                                                                                                                                                                                                                                                                                                                                           antifungal; fungal disease; acetohydroxyacid isomeroreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAARNCTKALRPLARQLATPAVQRRTFVAAASAVRASVAVKAVAAPARQQVRGVKTMDFA
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                                                                                                                                                                                                                                                                                                                                                                  89.2%; Score 1860; DB 9; 87.1%; Pred. No. 1.2e-169; ive 34; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 350; Conserv
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                                                                                                                                                                                                                                                                                                                                 Sequence 400 AA;
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fungi on, e.g. cereals, inhibitor of acetohydroxy acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 EATQSLYPLIGANGMDWYYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGSETQR 358
                                                                                                                                                                                                                            The present invention relates to a method for controlling fungal disease in crops by applying an inhibitor (1) of acetohydroxyacid isomeroreductase. (1) are used for curative or preventative treatment of a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or rape. The present sequence is an acetohydroxyacid isomeroreductase, used to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAARNCTKALRPLARQLATPAVQRRTFVAAASAVRASVAVKAVAAPARQQVRGVKTMDFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDAIQDGWVPGKNLFDVDEAISRGTIVMNLLSDAAQSETWPHIKPQITKGKTLYFSHGFS
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                                                                                                                                                                                                                                                                                                                                                                    89.0%; Score 1856; DB 6; Length 402;
86.8%; Pred. No. 2.8e-169;
iive 35; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      substrate inhibition; antibiotic; gene disruption; ketol-acid reductoisomerase; KAR1; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                    14;
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                                                                           Effantin G,
                                                                                                                                    Treatment of crops, useful for controlling potato, cotton or rape, comprises applying
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                                                                         Zundel JL,
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                                            (AVET ) AVENTIS CROPSCIENCE SA
               10-SEP-2001; 2001FR-00011689.
                                                                                                                                                                                                 Claim 2; Fig 1; 66pp; French.
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Matches 349; Conservative
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                                                                           Lebrun MH,
                                                                                                      WPI; 2003-405775/39
                                                                                                                                                                  isomeroreductase.
                                                                                                                                                                                                                                                                                                                                        Sequence 402 AA;
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Best Local S
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The invention describes a method of identifying a test compound as a candidate for an antibiotic comprising contacting ornithine carbamoytransferase (Ocrase) or ketol-acid reductoisomerase polypeptide, or fungal pathogenicity-conferring gene with a test compound. The method comprises: contacting Ocrase polypeptide, ketol-acid reductoisomerase polypeptide, or fungal pathogenicity-conferring gene with a test compound of expecting the presence or absence of binding between the test compound and the polypeptide or gene, where binding indicates that the compound and the polypeptide or gene, where binding indicates that the set compound at least 50% sequence identity to, or having at least 10% of the activity of, 400, 403 or 469 amino acids; and an isolated polypeptide consisting essentially of the amino acids and insolated polypeptide consisting essentially of the amino acids and insolated or 469 amino acids and fungal or 469 amino acids and fungal pathogenicity-conferring gene as antibiotics. This is the amino acid sequence of worder pathogenicity-conferring gene as antibiotics. This is the amino acid sequence of Mycosphaerella graminical ketol-acid reductoisomerase KARI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a test compound as a candidate for an antibiotic comprises contacting ornithine carbamoytransferase (OCTase) or ketol-acid reductoisomerase polypeptide, or fungal pathogenicity-conferring gene
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                                                                                                                                                                                                                                                          Shuster JR;
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                                                                                                                                                                                                                       Lo SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 1658; DB 9;
; Pred. No. 3.2e-150;
40; Mismatches 43;
                                                                                                                                                                                                                   Tanzer MM, Hamer L, Adachi K, Dezwaan TM, Lo
Montenegro-Chamorro MV, Darveaux BA, Frank SA,
Mahanty SK, Pan H, Covington AS, Tarpey R, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 50; SEQ ID NO 9; 179pp; English.
                                                                                                                                                                                                                                                                                                                    N-PSDB; ADV16802, ADV16808, ADV16809.
                                                                                                                                                                           (PARA-) PARADIGM GENETICS INC
                                                                                             15-MAY-2003; 2003US-0470947P.
19-MAY-2003; 2003US-0471615P.
21-MAY-2003; 2003US-0472242P.
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                                                       17-MAY-2004; 2004WO-US015404
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                  02-DEC-2004
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elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which parthogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes of Aspergillus fumigatus of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 396 AA;
                                                                                                                                                                                                                                                              240
59 PAGHKEEVHERADWPAEKLLDYFKNDTLALIGYGSQGHGQGLNLRDNGLNVIVGVRKNGK 118
                        61 FAGDKEKVFERDDWFREKLLEYFKNDTLALIGYGSQGHGQGLNLRDNGLNVIVGVRKGGA 120
                                                                                                  SWEDAIQDGWVPGKNLFDVDEAISRGTIVMNLLSDAAQSETWPHIKPQITKGKTLYFSHG 178
                                                                                                                                   FSPVFKDLTKVEVPTDVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEKAV 238
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                                                                                                                                                                                                                                                                                                                                                                                                                       VEEATQSLYPLIGAHGMDWMFDACSTTARRGAIDWTPKFKDALKPVFNNLYDSVKNGDER 358
                                                                                                                                                                                                                                        ALGVAVGSGYLYETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNET
                                                                                                                                                                                                                                                                                                                                             181
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic corganism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contemination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. iumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologues sesential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antibodies to a sign and antibodies, and for identifying polymucleotides encoding the other protein vith which binding occurs or to identify inhibitors of the binding of interaction. The polypeptides may be used to raise antibodies or to elict annibution of interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                              essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response.
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                 Hu W,
359 KRSLEYNSQPDYRERYEAELDEIRNLEIWRAGK--RSLRPEN
                                                                                                                                                                                                                                           Aspergillus fumigatus essential gene protein #1135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eroshkin AM,
                                                                                                                           ABJ26477 standard; protein; 396 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zamudio C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-APR-2001; 2001US-0287066P.
05-JUN-2001; 2001US-0295890P.
09-JUL-2001; 2001US-0303899P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-2002; 2002WO-US013142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                  cancer; contamination;
                                                                                                                                                                                                                                                                                cytostatic;
                                                                                                                                                                                                                                                                                                                                     Aspergillus fumigatus.
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                                                                                                                                                                                                                                                                              Fungicide;
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                                                                                   GKSWEDAIQDGWVPGKNLFDVDEAISRGTIVMNLLSDAAQSETWPHIKPQITKGKTLYFS 176
                                                                                                                                                  HGFSPVFKDLTKVEVPTDVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEK 236
                                                                                                                                                                                       AVALGVAVGSGYLYETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFN 296
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                                                                                                                                                                                                                                                                                                                                                                                                              fumigatus; infection;
                                                1 MAARNCTKALRPLARQLATPAVQRRTFVAAA----SAVRASVAVKAVAAPARQQVRGVKT
                    16;
  Length 396;
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                                                                                                                                                                                                                                                                           essential gene; Aspergillus fumigat
biofilm; antibody; immune response.
                    36; Indels
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Score 1633; DB 6;
Pred. No. 7.9e-148;
5; Mismatches 36;
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                   35;
78.3%;
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05-JUN-2001; 2001US-0295890P.
09-JUL-2001; 2001US-0303899P.
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                                                                                                                                                                                                                                                                                                                                                                      (first entry)
Query Match 78.3
Best Local Similarity 78.6
Matches 319; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            le; cytostatic;
contamination;
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                                                                                                                                                                                                                                                                                                                                                                                                            Fungicide;
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                                                                                                                                                                                                                                                                                                                                                                                                                      cancer;
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of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polymucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypoptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for
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               the invention are used to treat or pevent infections by pathogenic organism such as A. fundatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fundatus, or to prevent or inhibit formation on a surface of a captesing comprising A. fundatus. The polymuclectides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fundatus to identify duplicated genes or paralogues having the same or similar blochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologue sesential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an
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cancer; contamination; biofilm; antibody; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKSWEDAIQDGWVPGKNLFDVDEAISRGTIVMNLLSDAAQSETWPHIKPQITKGKTLYFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGFSPVFKDLTKVEVPTDVDV1LVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                           host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.3%; Score 1633; DB 6; Length 508; 78.6%; Pred. No. 1.2e-147; ive 35; Mismatches 36; Indels 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 78.6
nes 319; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 508 AA;
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purified or isolated nucleic acids of essential genes of Aspergillus igatus, useful for treating or preventing infections by A. fumigatus, for treating a non-infectious disease in a subject e.g. cancer.

New purified or isolated nucleic acids of

The invention relates to novel purified or isolated nucleic acids

Disclosure, Page, 175pp, English.

Lemieux SM;

Hu ₩,

Eroshkin AM,

Zamudio C,

2001US-0316362P

31-AUG-2001;

(ELIT-) ELITRA PHARM INC.

Jiang B, Tishkoff D,

WPI; 2003-093124/08.

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27-APR-2001; 2001US-0287066P.
05-JUN-2001; 2001US-0295890P.
09-JUL-2001; 2001US-0303899P.
                                23-APR-2001; 2001US-0285697P
                                              31-AUG-2001; 2001US-0316362P
                         23-APR-2002; 2002WO-US013142
   Aspergillus fumigatus
          WO200286090-A2
                  31-OCT-2002
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(ELIT-) ELITRA PHARM INC

Lemieux SM Hu W, Eroshkin AM, Zamudio C, Jiang B, Tishkoff D, WPI; 2003-093124/08 , purified or isolated nucleic acids of essential genes of Aspergillus nigatus, useful for treating or preventing infections by A. fumigatus, for treating a non-infectious disease in a subject e.g. cancer.

Disclosure; Page; 175pp; English

The invention relates to novel puritise or isolated nucleic acids of essential genes of Aspergillus funiqatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic corganism such as A. funigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contamination of an object by A. fumigatus, or to prevent or contamination of an object by A. fumigatus, or to prevent or contamination of an object corpusion of an object corpusion of an object corpusion of the funigatus. The polymorlectides are useful for expressing recombinant protein for characterisation, screening or characterisation, screening or characterisation, screening or corganisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential or virulence genes, for selecting and conting on to raise anti-DNA antibodies or to elicit another immune response, and for identifying polymucleotides encoding the other protein crapsonse, and for identifying polymucleotides encoding the other protein crapsonse, and for identifying polymucleotides encoding the other protein crapsonse, and for identifying polymucleotides encoding the other protein crapsonse, and for identifying polymucleotides encoding the other for elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to issolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes or of Aspergillus fundagatus of the invention invention relates to novel purified or isolated nucleic acids of

Sequence 388 AA;

MDFAGHKEEVHERADWPAEKLLDYFKNDTLALIGYGSQGHGQGLNLRDNGLNVIVGVRKN 116 117 GKSWEDAIQDGWVPGKNLFDVDEAISRGTIVMNLLSDAAQSETWPHIKPQITKGKTLYFS 176 HGFSPVFKDLTKVEVPTDVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEK 236 26 20 MAARNCTKALRPLARQLATPAVQRRTFVAAA----SAVRASVAVKAVAAPARQQVRGVKT Gaps 14; 76.9%; Score 1604; DB 6; Length 388; 78.7%; Pred. No. 4.7e-145; ive 35; Mismatches 35; Indels 1 Best_Local Similarity 78.7 Matches 311, Conservative Query Match g 쉽 ò ò

291 ETVEEATQSLYPLIGANGMDWMYAACSTTARRGAIDWSSRFKDTLKPIFNELYDSVRDGT 350 237 AVALGVAVGSGYLYETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFN ETVERATQSLYPLIGAHGMDWMFDACSTTARRGAIDWTPKFKDALKPVFNNLYDSVKNGD 351 ETKRSLEYNSQKDYREKYEKEMQDIRDLEIWRAGK 385 357 ERKRSLEYNSQPDYRERYEAELDEIRNLEIWRAGK 391 297 à 셤 à 셤 ò 셤

Fungicide, cytostatic, essential gene, Aspergillus fumigatus, infection, cancer, contamination, biofilm, antibody, immune response. Aspergillus fumigatus essential gene protein #535. ABJ25877 standard; protein; 500 AA Aspergillus fumigatus 16-APR-2003

23-APR-2002; 2002WO-US013142. WO200286090-A2 31-OCT-2002

23-APR-2001; 2001US-0285697P. 27-APR-2001; 2001US-0287066P. 05-JUN-2001; 2001US-029890P. 09-JUL-2001; 2001US-031899P. 31-AUG-2001; 2001US-0316362P.

Zamudio C, (ELIT-) ELITRA PHARM INC. Tishkoff D, Jiang B,

New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer. WPI; 2003-093124/08.

Hu W,

Eroshkin AM,

Disclosure; Page; 175pp; English.

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with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to fasolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes of Aspergillus fumigatus of the invention
                                                                                                                                                                                                               HGFSPVFKELTKVDVPKDVDVLLVAPKGSGRTVRTLFREGRGINSSIAVYQDVTGKAKEK 342
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                                                                                                                                                                         Gaps
                                                                                                                                                                         14;
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                                                                                                                                              Length 500;
                                                                                                                                                                        35; Indels
                                                                                                                                           76.9%; Score 1604; DB 6; 78.7%; Pred. No. 6.9e-145; iive 35; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERKRSLEYNSQPDYRERYEAELDEIRNLEIWRAGK 391
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                                                                                                                                                                      Matches 311; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene replacement and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roemer T, Jiang B,
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N-PSDB; AAS23417.
                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Candida albicans
                                                                                                                     Sequence 500 AA;
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                                                                                                                                              Query Match
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strains useful for identification and validation of gene products as targets for therapeutic agents, for creating a collection of identified essential genes, and screening assays for the discovery of new drugs. The invention provides the GRACE (gene replacement and conditional expression) method for the construction of mutant organisms referred to as GRACE strains of the organism. The invention can be applied to any organism, particularly a pathogenic fungus e.g. Candida albicans, Aspergillus fumigatus and Cryptococcus neoformans. The methods are useful to identify agents that may be used in the treatment of fungal infections. AAU15053-AAU15113 represent proteins encoded by C. albicans
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                                                                                              invention relates to novel methods for constructing fungal
                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAARNCTKALRPLARQLATPAVQRRTFVAAASA----VRASVAVKAVAAPARQQVRGVKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 MDFAGHKEEVHERADWPAEKLLDYFKNDTLALIGYGSQGHGQGLNLRDNGLNVIVGVRKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGFSPVFKDLTKVEVPTDVDV1LVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEK
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               and identifying
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signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal.
                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                          4; Length 400;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
               Identifying genes essential to fungal metabolisms and potential therapeutic agents that target these genes
                                                                                                                                                                                                                                                                                                                                                                          51;
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                                                                                                                                                                                                                                                                                                                                          73.8%; Score 1539.5; DB 4, 73.1%; Pred. No. 7.9e-139; ive 47; Mismatches 51;
                                                              Claim 43; Page 222-223; 324pp; English
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                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 296; Conserv
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                                                                                                                                                                                                                                                                                                           Sequence 400 AA;
                                                                                                                                                                                                                                                                              essential genes
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Matches
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357 ERKRSLEYNSQPDYRERYEAELDEIRNLEIWRAGK--RSLRPENQ 399

356 ETKRSLEFNSRSDYKERLEEELQTIRNMEIWRVGKEVRKLRPENQ

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Ohlsen KL;

Bussey H,

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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by insertions or promoter replacement fragment with a heterologous recombination, of a promoter replacement fragment with a heterologous promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene that expression both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus to an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon capound catabolism, biosynthetic, transporter, transcriptional, translational, signal transduction, DNA replication and cell division compound catabolism, biosynthetic, transporter, transcriptional, translational, signal transduction, DNA replication and cell division compound so thinbibit growth or proliferation of C. albicans cells and cessential C. albicans related a brinted abbicans protein used in the method of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                 Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 44; SEQ ID NO 7075; 167pp + Sequence Listing; English
                                                                                                                                                                                                                Boone C,
                                                                                          20-FEB-2001; 2001US-00792024, 22-AUG-2001; 2001US-0314050P.
                      26-DEC-2001; 2001WO-US049486
                                                                      2000US-0259128P
                                                                                                                                                                (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                Jiang B,
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                                                                   29-DEC-2000;
                                                                                                                                                                                                                Roemer T,
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57 MDFAGHKEEVHERADWPAEKLIDYFKNDTLALIGYGSQGHGQGLNLRDNGLNVIVGVRKN 116 HGFSPVFKDLTKVEVPTDVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEK 236 AVALGVAVGSGYLYETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFN 296 ETVEEATQSLYPL1GAHGMDWMFDACSTTARRGAIDWTPKFKDALKPVFNNLYDSVKNGD 356 117 GKSWEDAIQDGWVPGKNLFDVDEAISRGTIVMNLLSDAAQSETWPHIKPQITKGKTLYFS 1 MAARNCTKALRPLARQLATPAVQRRTFVAAASA----VRASVAVKAVAAPARQQVRGVKT Gaps 11; 5; Length 400; 51; Indels Score 1539.5; DB 5 Pred. No. 7.9e-139; 47; Mismatches 73.8%; 73.1%; Query Match 73.8 Best Local Similarity 73.1 Matches 296; Conservative 237 177 셤 Š g ઠે 셤 ò 셤 8 요

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method for controlling fungal disease in crops by applying an inhibitor (I) of acetohydroxyacid isomeroreductase. (I) are used for curative or preventative treatment of a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or rape. The present sequence is an acetohydroxyacid isomeroreductase, used to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
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                                                                                                                      Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDAIQDGWVPGKNLFDVDEAISRGTIVMNLLSDAAQSETWPHIKPQITKGKTLYFSHGFS
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73.6%; Pred. No. 7.4e-136;
ive 39; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                   Effantin G,
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                                                                                             Acetohydroxyacid isomeroreductase.
                                                                                                                                                                                                                                                                                                                                 Zundel JL,
           ABR64304 standard; protein; 395
                                                                                                                                                                                                                                                                                                        (AVET ) AVENTIS CROPSCIENCE SA.
                                                                                                                                                                                                                                                 10-SEP-2001; 2001FR-00011689.
                                                                                                                                                                                                                                                                            10-SEP-2001; 2001FR-00011689.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Fig 1; 66pp; French.
                                                                                                                                                                 Saccharomyces cerevisiae.
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Matches 295; Conservative
                                                                                                                                                                                                                                                                                                                                   Lebrun MH,
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                                                                  16-SEP-2003
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                                      ABR64304
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Best Local S
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ABR64304
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17; Gaps

Indels

50;

39; Mismatches

Conservative

295;

Matches

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The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that in the specification. The variants are encoded by nucleic acids that hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are particularly agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful con screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein consponents of the complex is useful for the manufacture of a medicament or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was
                                                    EATOSLYPLICAHGMDWMFDACSTTARRGAIDWTPKFKDALKPVFNNLYDSVKNGDERKR 360
New proteins and protein complexes from eukaryotes, useful as targets in drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G, Kuester B, Schultz J;
Kruse U, Merino A, Bauch A;
                                                                                                                         SLEYNSOPDYRERYEAELDEIRNLEIWRAGK--RSLRPENG 399
                                                                                                                                          Disease treating protein complex-derived protein #1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 2561; 13pp; English
                                                                                                                                                                                                                                                                                                                                                                                      protein complex; drug target; diagnosis.
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P, Krause R,
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Marzioch M, Grandi P, Krause k
"'..hon A, Leutwein C, Rick J;
                                                                                                                                                                                                                                              ADK64188 standard; protein; 395
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                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorder in a subject.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1338608-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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                                                                                                                                                                                      PVFKDLTKVEVPTDVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEKAVAL 240
                                                                                                                                                                                                                                                     300
                                                              GHKEEVHERADWPAEKLLDYFKNDTLALIGYGSQGHGQGLNLRDNGLNVIVGVRKNGKSW 120
                                                                                                                        EDAIQDGWVPGKNLFDVDEAISRGTIVMNLLSDAAQSETWPHIKPQITKGKTLYFSHGFS 180
                                                                                                                                                         174
                                                                                                                                                                                                                      234
                                                                                                                                                                                                                                                                     235 AVAIGSGYVYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVE 294
                                                                                                                                                                                                                                                                                                                                 295 BALGSLYPLIGKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKR 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel purified or isolated Cryptococcus neoformans nucleic acid molecule comprising a sequence encoding a polypeptide comprising a sequence not given in the specification. A polymucleotide of the invention has fungicide activity, and may have a use in gene therapy. The nucleic acid is useful for preparing a use in gene treating an infection caused by Cryptococcus neoformans. The present sequence represents a C. neoformans sequence of the invention. Note: The sequence data for this patent is not represented in
 9
                   GTVETVYERADWPREKLLDYFKNDTFALIGYGSQGYGQLMLRDNGLNVIIGVRKDGASW
                                                                                                                                                                                                        175 PVFKDLTHVEPPKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQAL
                                                                                                                                           7 TKALRPLARQLATPAVQRRTFVAAASAVRASVAVKAVAAPARQQV-----RGVKTMDFA
                                                                                                                                                                                                                                                     GVAVGSGYLYETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVE
                                                                                                                                                                                                                                                                                                                  EATQSLYPLIGAHGMDWMFDACSTTARRGAIDWTPKFKDALKPVFNNLYDSVKNGDERKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid, useful for preparing a composition for treating an infection caused by Cryptococcus neoformans.
                                                                                                                                                                                                                                                                                                                                                                                                 355 SLEFNSQPDYREKLEKELDTIRNMEIWKVGKEVRKLRPENQ 395
                                                                                                                                                                                                                                                                                                                                                                                361 SLEYNSQPDYRERYEAELDEIRNLEIWRAGK--RSLRPENQ 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C. neoformans amino acid sequence SEQ ID NO:3168.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fungicide, gene therapy; infection
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Length 395;

Score 1508.5; DB 7; Pred. No. 7.4e-136;

72.3%; 73.6%;

Query Match Best Local Similarity us-10-797-248a-3.rag

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the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.
                                                                                                                                     HKEEVHERADWPAEKLLDYFKNDTLALIGYGSQGHGQGLNLRDNGLNVIVGVRKNGKSWE 121
                                                                                                                                                DAIQDGWVPGKNLFDVDEAISRGTIVMNLLSDAAQSETWPHIKPQITKGKTLYFSHGFSP 181
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                                                                                                                                                                                                                                                                                                          ATOSLYPLIGAHGMDWMFDACSTTARRGAIDWTPKFKDALKPVFNNLYDSVKNGDERKRS 361
                                                                                                                                                                                                                                                                                                                      screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             essential gene; cell proliferation; drug design
                                                                                                         VFKDLTKVEVPTDVDVILVAPKGSGRTVRSLFREGRGINSSFAVYQDVTGKAKEKAVALG
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                                                                                            3 ARNCTKALRPLARQLATPAVORRTF-VAAASAVRASVAVKAVAAPARQQVRGVKTMDFAG
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Xu HH;
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                                                   68.2%; Score 1423.5; DB 7; Length 409; 70.2%; Pred. No. 1.2e-127;
                                                                        62; Indels
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LEFNSRKTYREDLQKELDEIDNQEIWRAGKTVRGLR 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haselbeck R,
Yamamoto R,
                                                                        47; Mismatches
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Carr GJ,
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06-SEP-2001, 2001US-0094893.
25-OCT-2001, 2001US-0342921P.
08-FEB-2002, 2002US-00072851.
06-MAR-2002, 2002US-0362699P.
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                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prokaryotic
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Trawick JD,
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es 278; Conserv
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                               Sequence 409
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide (5) producing the polypeptide of specifically binding the polypeptide (5) producing the polypeptide; (6) inhibiting cellular croproliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for croproliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological corpusion a gene required for cellular proliferation of identifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the sene corpusion of strains; or (13) identifying the target of a compound that inhibits the extent compound that inhibits proliferation of a strains; or (13) identifying proteins or screening for homologous nucleic acids are useful for dence of for cellular proliferation of an organism. The antisense nucleic acids are useful for for confound in a conformance or for severations or for confound confound that inhibits are confound and confound actional actions or for confound and confound action of an organism. The antisense nucleic acids are useful for for cellular proliferation to solate candidate molecules for rational and antisement and acids are useful for an action of an organism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 MDFAGHKEEVHERADWPAEKLLDYFKNDTLALIGYGSQGHGQGLNLRDNGLNVIVGVRKN 116
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  to
for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.
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                                                                      SEQ ID NO 48900; 1766pp; English.
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                                                                           Claim 25;
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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

March 22, 2006, 15:21:02; Search time 113.517 Seconds (without alignments) 1528.885 Million cell updates/sec

- protein search, using sw model

OM protein

Run on:

US-10-797-248A-2 Title: Perfect score:

2071 1 MLRIQAARLICNSRVITAKR.....RNMEIWKVGKEVRKLRPENQ/395, Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 seqs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s: Geneseq 21 Database :

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2005s:* geneseqp2000s:* geneseqp2002s: geneseqp1990s: geneseqp2001s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Abr64304 Acetohydr	Adk64188 Disease t	Aau15089 Protein e	Abp73238 Candida a	Abr64305 Acetohydr	Abr64306 Acetohydr	Adv16807 M grisea		Abj26477 Aspergill			Abj25877 Aspergill		Adb70124 C. neofor	Abu20976 Protein e	Aab96356 Putative	Abu24174 Protein e	Abb48168 Listeria	Abu32456 Protein e	Aau01250 B. subtil	Aag81458 S. epider	Abu42920 Protein e	Abp39068 Staphyloc	
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SUMMARIES																										
		į	304	188	089	238	302	306	807	303	477	502	902	877	810	124	916	326	174	168	456	250	458	920	990	053
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		Score	2071	2071	1667	1667	1508.5	1507	1507	1503	1487.5	1487.5	1462.5	1462.5	1448.5	1392, 5	1099.5	495	470	465	465	461	458.5		458.5	458.5
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ADM26226 ABU18526 AAU34233	AAU36568 ABU16517 ABU43732 ABP77403	ABB92723 ADT55519 ABU44602 ABW70806	ABU3 8085 ABU3 8085 ABB 19104 AAY 5182	ABU25629 AAG26356 AAU37780	AAU38003 ABU00804 ABU45897
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25 26 27	28 30 31	3 3 3 3 2	1 4 4 4 4 6 4 4 6 4 4 6 4 6 4 6 4 6 4 6	0 4 4 4 0 1 2	4 4 4 6 4 7

ALIGNMENTS

ABR64304 standard; protein; 395 AA. RESULT 1 ABR64304

ABR64304;

16-SEP-2003 (first entry)

Acetohydroxyacid isomeroreductase.

Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase;

Saccharomyces cerevisiae

FR2829363-A1.

14-MAR-2003.

10-SEP-2001; 2001FR-00011689

10-SEP-2001; 2001FR-00011689

(AVET) AVENTIS CROPSCIENCE SA.

Zundel JL, Effantin G, Lebrun MH, WPI; 2003-405775/39 Dumas R,

Morin V;

Treatment of crops, useful for controlling fungi on, e.g. cereals, potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid isomeroreductase.

Claim 2; Fig 1; 66pp; French.

The present invention relates to a method for controlling fungal disease in crops by applying an inhibitor (I) of acetohydroxyacid isomeroreductase. (I) are used for curative or preventative treatment of a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or rape. The present sequence is an acetohydroxyacid isomeroreductase, used to illustrate the invention

Sequence 395 AA;

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Gaps ; 0 Length 395; 0; Indels Query Match 100.0%; Score 2071; DB 6; Best Local Similarity 100.0%; Pred. No. 1.3e-186; Matches 395; Conservative 0; Mismatches 0;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that hybridize to the nucleic acids encoding the proteins under low stringency
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                                                                                                      GWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGKTLYFSHGFSPVFKDL 180
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                                                         YERADWPREKLLDYFKNDTFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWKAAIED
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                         MIRTQAARLICNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETV
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           MLRTQAARLICNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETV
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Or
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drug screening, or in diagnosing or screening for the presence of
disease or disorder, or a predisposition for developing a disease
disorder in a subject.
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P, Krause R, Kruse U, Merino A, Bauch
                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein #1281.
                                                                                                                                                                                                                                                                                                         QPDYREKLEKELDTIRNMEIWKVGKEVRKLRPENQ 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating protein complex-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein complex; drug target; diagnosis.
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Leutwein C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gavin A,
M, Grandi
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N-PSDB; ADK64189.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
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              agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament for the treatment or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).
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                                                                                                                                                                                                                                                                                                                                                                 Length 395;
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                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 2071; DB 7;
100.0%; Pred. No. 1.3e-186;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     are useful as
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                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                    Sequence 395 AA;
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Matches
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Candida albicans.
                       WO200253728-A2
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                                                                                                                                strains useful for identification and validation of gene products as targets for therapeutic agents, for creating a collection of identified sessential genes, and screening assays for the discovery of new drugs. The invention provides the GRACE (gene replacement and conditional expression) method for the construction of mutant organisms referred to organism. The invention can be applied to any organism, particularly a pathogenic fungus e.g. Candida albicans, Aspergillus funigatus and Cryptococcus neoformans. The methods are useful to identify agents that may be used in the treatment of fungal infections. AAUIS053-AAUIS113 represent proteins encoded by C. albicans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDLTHVEPPKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVA 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSLYPLIGKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLE 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSLYPLIGKYGMDYMYDACSTTARRGALDWYPRFKDALKPVFEELYESVKNGSETKRSLE 362
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                                                                                                                                                                                                                                                                                                                                                           3 RIOAARL--ICNSRVITAKRIFAL---ATRAAAYSRPAARFVKPMITTRGLKQINFGGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Gaps
                                                                 Identifying genes essential to fungal metabolisms and identifying potential therapeutic agents that target these genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fungus, yeast, tetracyclin, promoter, GRACE strain, blosynthesis,
signal transduction, DNA replication, cell division, growth,
proliferation, Candida albicans, fungicide, antifungal.
                                                                                                                          to novel methods for constructing
                                                                                                                                                                                                                                                                                                 80.5%; Score 1667; DB 4; Length 400; 79.1%; Pred. No. 2.2e-148; ive 42; Mismatches 35; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FNSQPDYREKLEKELDTIRNMEIWKVGKEVRKLRPENQ 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Candida albicans essential protein SEQ ID NO 7075.
           Bussey H;
                                                                                                    Claim 43; Page 222-223; 324pp; English.
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                                                                                                                          The present invention relates
           Boone C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                           Best Local Similarity 79.1
Matches 315; Conservative
          Jiang B,
                                 2001-489080/53
                                            N-PSDB; AAS23417
                                                                                                                                                                                                                                                                            Sequence 400 AA;
                                                                                                                                                                                                                                                      essential genes
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           Roemer T,
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The invention relates to constructing (MI) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by insertion or replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (MI) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells in which both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian agent, an antifungal agent for treatment of a mammalian compound catabolism, blosynthetic, transporter, transcriptional, compound catabolism, blosynthetic, transporter, transcriptional, compound catabolism, blosynthetic, transporter, transcriptional, contributery is signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and cell and essential Candida albicans protein used in the method of the invention. Note: The sequence data for this patent is not represented in the printed by the present of the present sequence of the present by the property of the pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 44; SEQ ID NO 7075; 167pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohlsen KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bussey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boone C,
                                                                                                                                                                                 29-DEC-2000; 2000US-0259128P.
20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
                                                                                           26-DEC-2001; 2001WO-US049486
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Matches 315; Conservative
                                                                                                                                                                                                                                                                                                                                                                            (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roemer T, Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-566694/60.
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11-JUL-2002
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241 GVAVGSGYLYETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVE
                                  235 AVAIGSGYVYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVE
                                                                             EATQSLYPLIGKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treatment of crops, useful for controlling potato, cotton or rape, comprises applying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 57-58; 66pp; French.
                                                                                                                                                                                                                                                                          Acetohydroxyacid isomeroreductas #2.
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                                                                                                                                                                                                     ABR64306 standard; protein;
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                                                                                                                                                                                                                                                   (first entry)
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Best Local Similarity 73.2
Matches 289; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lebrun MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2003-405775/39
                                                                                                                                                                                                                                                                                                                     Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isomeroreductase.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treatment of crops, useful for controlling fungi on, e.g. cereals, potato, cotton or rape, comprises applying inhibitor of acetchydroxy acid isomeroreductase.
                      302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GHKEEVHERADWPAEKLLDYFKNDTLALIGYGSQGHGQGINLRDNGLNVIVGVRKNGKSW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 KAAIEDGWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGKTLYFSHGFS 174
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            IGSGYVYKTTFEREVNSDLYGERGCLMGGIHGMFLAQYEVLRENGHTPSEAFNETVEEAT
                                          QSLYPLIGKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLE
                                                                                                                                                                                                                                                           Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Morin V;
                                                                                                 FNSQPDYREKLEKELDTIRNMEIWKVGKEVRKLRPENQ 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.8%; Score 1508.5; DB (73.6%; Pred. No. 2.1e-133.1ive 39; Mismatches 50.
                                                                                                                                                                                                                                                                                                                                                                                                                        Effantin G,
                                                                                                                                                                   ABR64305 standard; protein; 400 AA
                                                                                                                                                                                                                                     Acetohydroxyacid isomeroreductase
                                                                                                                                                                                                                                                                                                                                                                                                                       Zundel JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Fig 1; 66pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                (AVET ) AVENTIS CROPSCIENCE
                                                                                                                                                                                                               (first entry)
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Best Local Similarity 73.6
Matches 295; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Lebrun MH,
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                                                                                                                                                                                                                                                                                   Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 400 AA;
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                             301 EATQSLYPLIGAHGMDWMFDACSTTARRGAIDWTPKFKDALKPVFNNLYDSVKNGDERKR 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.
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                                                                                                                                                       SLEYNSQPDYRERYEAELDEIRNLEIWRAGK--RSLRPENQ 399
                                                                                                                       SLEFNSQPDYREKLEKELDTIRNMEIWKVGKEVRKLRPENQ 395
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Sequence 400 AA;
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                                                                                                                                                  300
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244
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                                                                                                                                                                                                                                                       305 YPLIGANGMDWMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVXDGSETQRSLDYNS 364
                                                                                          THVEPPKOLDVILVAPKGSGRTVRSLPKEGRGINSSYAVWNDVTGKAHEKAQALAVAIGS
                                                                                                                                                GYVYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEATQSL
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contacting ornithine carbamoytransferase (OCTase) or ketol-acid
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SA, Heiniger RW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibition; antibiotic; gene disruption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contacting ornithine carbamoytransferase (OCTase)
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                                                                                                                                                                                                                                                                                                                 QPDYREKLEKELDTIRNMEIWKVGKEVRKLRPENQ 395
                                                                                                                                                                                                                                                                                                                                         QPDYREKYEAEMEEIRNLEIWRAGKAVRSLRPENQ 399
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ington AS, Tarpey R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dezwaan TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ketol-acid reductoisomerase; ILV5; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 48; SEQ ID NO 6; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Montenegro-Chamorro MV, Darveaux E
Mahanty SK, Pan H, Covington AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADV16807 standard; protein; 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adachi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PARA-) PARADIGM GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-2003; 2003US-0470947P.
19-MAY-2003; 2003US-0471615P.
21-MAY-2003; 2003US-0472242P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-021202/02.
N-PSDB; ADV16805, ADV16806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hamer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a test compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        grisea ketol-acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004104176-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              substrate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
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of
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                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                            64
polypeptide consisting essentially of the amino acid sequence of 400, 4 or 469 amino acids. The methods are useful for identifying inhibitors cornithine carbamoytransferase, ketol-acid reductoisomerase, and fungal pathogenicity-conferring gene as antibiotics. This is the amino acid sequence of Magnaporthe grisea ketol-acid reductoisomerase ILVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 GWVPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPALKPQITKGKTLYFSHGFSPVFKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 WERADWPKEKILIEYFKDDTLALIGYGSQGHGQGLNLRDNGLNVIIGVRKDGKSWKDAVQD
                                                                                                                                                                                                                                                                                                                                        2 LRTQAARLICNSRVITAKRTFALATRAAAYSRPAARFVKP-MITTRGLKQINFGGTVETV
                                                                                                                                                                                                                                                                                                                                                                                            LRPMARQL---ATPAVQRRTFVAASSMVRATRKAA--VAPTQQQIRGVKTMDFAGHKEQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGKTLYFSHGFSPVFKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THVEPPKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVAIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKVEVPTDVDVILCAPKGSGRTVRSLFREGRGINSSFAVYQDVTGEAEEKAIALGVAIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYVYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEATQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 GYLYKTTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVERATQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YPLIGKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                          Length 400;
                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                          72.8%; Score 1507; DB 9; 73.2%; Pred. No. 2.9e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QPDYREKLEKELDTIRNMEIWKVGKEVRKLRPENQ 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Effantin G,
                                                                                                                                                                                                                                                                                 44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acetohydroxyacid isomeroreductase #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402
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                                                                                                                                                                                                                                                                                    Matches 289; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-405775/39
                                                                                                                                                                                                                                                          Similarity
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              The present invention relates to a method for controlling fungal disease in crops by applying an inhibitor (I) of acetohydroxyacid isomeroreductase. (I) are used for curative or preventative treatment of a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or rape. The present sequence is an acetohydroxyacid isomeroreductase, used to illustrate the invention
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                                                                                                                                                                                                                                                                                             YPLIGKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFNS 360
                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                        essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response.
                                                                                                                                                                    GWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGKTLYFSHGFSPVFKDL
                                                                                                                                                                                                                                                              GYVYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEATQSL
                                                                                                                                                           61 YERADWPREKLLDYFKNDTFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWKAAIED
                                                                                                                                                                                                                             THVEPPKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVAIGS
                                                                                                                          LRTQAARLICNSRVITAKRTFALATRAAAYSRPAARFVKP-MITTRGLKQINFGGTVETV
                                                                                                            Gaps
                                                                                                           9
                                                                                            Length 402,
                                                                                                           56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Aspergillus fumigatus essential gene protein #1135.
                                                                                         72.6%; Score 1503; DB 6; 72.9%; Pred. No. 7.1e-133;
                                                                                                                                                                                                                                                                                                                             OPDYREKLEKELDTIRNMEIWKVGKEVRKLRPENQ 395
                                                                                                                                                                                                                                                                                                                                         45; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                      ABJ26477 standard; protein; 396
Claim 2; Fig 1; 66pp; French.
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27-APR-2001; 2001US-0287066P.
05-UUN-2001; 2001US-029899P.
09-UUL-2001; 2001US-031899P.
31-AUG-2001; 2001US-0316362P.
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                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                          Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer; contamination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aspergillus fumigatus
                                                                                                  Similarity
                                                                         Sequence 402 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fungicide;
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                                                                                          Query Match
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a bofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid ariza, for examination or a paralog and arizay for examination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polymuclectides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypoptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes
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                                                                                                                                 * purified or isolated nucleic acids of essential genes of Aspergillus
nigatus, useful for treating or preventing infections by A. fumigatus,
for treating a non-infectious disease in a subject e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 VPKDVDVILVAPKGSGRTVRTLFREGRGINSSIAVYQDVTGKAKEKAIAMGVAVGSGYLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 ETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEATQSLYPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 QAARLICNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETVYERA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFNSQPDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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       Lemieux SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
       3
       H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.8%; Score 1487.5; DB 6; 71.6%; Pred. No. 2e-131; ive 46; Mismatches 62;
       Eroshkin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REKLEKELDTIRNMEIWKVGKEVRKLRPENQ 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of Aspergillus fumigatus of the invention
   Zamudio C,
                                                                                                                                                                                                                                                                                Disclosure; Page; 175pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 71.6
Matches 280; Conservative
Tishkoff D,
                                                                    WPI; 2003-093124/08.
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                                                                                                                                        New purified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65
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DWPREKLLDYFKNDTFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWKAAIEDGWVP

65 177 125

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124

120 RALRL---ARVAAPRTVISAALPRPALAKAATRVAASTAPVRGVKTIAFADSKETVYERA 176

GKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGKTLYFSHGFSPVFKDLTHVE 184

244 356 476

REKLEKELDTIRNMEIWKVGKEVRKLRPENQ

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ABJ25902 standard; protein; 388

RESULT 11

ABJ25902

416 364

QTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEATQSLYPLI 304

GKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFNSQPDY

297 VPKDVDVILVAPKGSGRTVRTLFREGRGINSSIAVYQDVTGKAKEKAIAMGVAVGSGYLY

PPKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVAIGSGYVY

185

245 357 305 417 365

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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat a non-infectious by a pathogenic organism such as A. fumigatus, to treat a non-infectious by apthogenic organism such as A. fumigatus, to prevent or contain contamination of an object blofilm comprising A. fumigatus The polynucleotides are useful for expressing recombinant protein for characterisation, screening or comparising A. fumigatus of the polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for ralsing anti-protein antibodies, as an anti-DNA antibodies or to elicit another immune cresponse, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding circurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively cettering timenum electron which pathogenic organism invade or reside, and to be determine levels of the protein in biological fluids, as a marker for the factors. This sequence represents a protein of eace or virulence of accors. This sequence represents a protein of eace or virulence of accorselative receptors or ligands in the case or virulence.
                                                                                                                                                                                                        Fungicide, cytostatic, essential gene, Aspergillus fumigatus, infection, cancer, contamination, biofilm, antibody, immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lemieux SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.8%; Score 1487.5; DB 6; Length 71.6%; Pred. No. 3e-131; ive 46; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hu W,
                                                                                                                                                           Aspergillus fumigatus essential gene protein #1160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eroshkin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Aspergillus fumigatus of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zamudio C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page; 175pp; English.
                       ABJ26502 standard; protein; 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-2001; 2001US-0285697P.
27-APR-2001; 2001US-0287066P.
05-UUN-2001; 2001US-029890P.
09-UUL-2001; 2001US-031899P.
31-AUG-2001; 2001US-0316362P.
                                                                                                                                                                                                                                                                                                                                                                                                                   23-APR-2002; 2002WO-US013142
                                                                                                             (first entry)
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Best Local Similarity 71.69
Matches 280; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tishkoff D,
                                                                                                                                                                                                                                                                           Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-093124/08.
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                                                                                                                                                                                                                                                                                                                      WO200286090-A2.
                                                                                                                16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2002
                                                                  ABJ26502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jiang B,
ABJ26502
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essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response.

Aspergillus fumigatus essential gene protein #560.

cancer; contamination; Fungicide, cytostatic,

Aspergillus fumigatus.

WO200286090-A2.

31-OCT-2002

(first entry)

16-APR-2003

ABJ25902;

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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a biofillm comprising A. fumigatus. The polynucleotides are useful for
                                                                                                                                                                                                                                                                                                                                     Lemieux SM;
                                                                                                                                                                                                                                                                                                                                     Hu W,
                                                                                                                                                                                                                                                                                                                                    Eroshkin AM,
                                                                                                                                                                                                                                                                                                                                     Zamudio C,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page, 175pp, English.
                                                                                                                                                                                                                                               27-APR-2001; 2001US-0287066P.
05-JUN-2001; 2001US-0295890P.
09-JUL-2001; 2001US-0303899P.
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                                                                                                                                                                                                                                                                                    31-AUG-2001; 2001US-0316362P
                                                                                                                                                                                                                                                                                                             (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                    Tishkoff D,
                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-093124/08.
                                                                                                                                                                                                                                                                                                                                    Jiang B,
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And Control Section

64

Gaps

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DB 6; Length 508;

QAARLICNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETVYERA

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SM;

Lemieux

Hu W,

Eroshkin AM,

Zamudio C,

WPI; 2003-093124/08.

Jiang B,

27-APR-2001; 2001US-0287066P. 05-JUN-2001; 2001US-0295890P. 09-JUL-2001; 2001US-0303899P. 31-AUG-2001; 2001US-0316362P.

(ELIT-) ELITRA PHARM INC. Tishkoff D,

23-APR-2002; 2002WO-US013142

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therapeutic use, as markers for host tissues in which the pathogenic corganisms invested or reaide, for comparing with the DNA sequence of A. funigatus to identify duplicated genes or paralogues having the same or funigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA comparing other related or distant pathogenic organisms to identify optential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune cresponse, and for identifying polymucleotides encoding the other protein with binding occurs or to identify inhibitors of the binding of interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes constants.
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Sequence 388 AA;

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DWPREKLLDYFKNDTFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWKAAIEDGWVP 124
                                                                                                                GKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGKTLYFSHGFSPVFKDLTHVE 184
                                                                                                                                                              244
                                                                                                                                                                                                             OTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEATQSLYPLI 304
                                                                                                                                                                                                                                                           GKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFNSQPDY 364
                                                                                                                                                                                                                                                                                                          64
                                                                              64
                                                                           8 RALRL---ARVAAPRTVISAALPRPALAKAATRVAASTAPVRGVKTIAFADSKETVYERA
                                                      QAARLICNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETVYERA
                                                                                                                                                                                                 185 PPKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVAIGSGYVY
                                Gaps
                              3;
        DB 6; Length 388;
                              60; Indels
       ; Score 1462.5; DB (
; Pred. No. 4.5e-129; 
46; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                          REKLEKELDTIRNMEIWKVGKEVR 388
                                                                                                                                                                                                                                                                                                                                                         365 REKYEKEMQDIRDLEIWRAGKAVR 388
       70.6%;
71.6%;
Query Match
Best Local Similarity 71.67
Marches 275; Conservative
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essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response. Aspergillus fumigatus essential gene protein #535. Ş ABJ25877 standard; protein; 500 (first entry) Pungicide; cytostatic; cancer; contamination; Aspergillus fumigatus 16-APR-2003 ABJ25877; RESULT 12 ABJ25877 BXBXBXEXBXIX

WO200286090-A2

31-OCT-2002

The invention relates to nover purities or isolated nucleic acids of essential genes of Aspergillus fungatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic corganism such as A. funigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or inhibit formation on a surface of a blofilm comprising A. funigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or corganisms invede or reside, for comparing with the DNA sequence of A. funigatus to identify duplicated genes or paralogues having the same or funigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA corganisms invede or reside, for distant pathogenic organisms of identify optermial orthologuus essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an engent or resides or identifying polynucleotides encoding the other protein antigen to raise anti-DNA antibodies or to elicit another immune corresponse, and for identifying polynucleotides encoding the other protein cinteraction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively conteraction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively conteraction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively conteraction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively contential manula protein of encorrelative receptors or ligands in the case or virulence or factors. This sequence represents a protein of one of the essential genes New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer. The invention relates to novel purified or isolated nucleic factors. This sequence represents a protes of Aspergillus fumigatus of the invention Disclosure; Page; 175pp; English.

Sequence 500 AA;

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                                                                                                                                                                                                                         GKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGKTLYFSHGFSPVFKDLTHVE 184
                                                                                                                                                                                                                                                                                                                                              304
                                                                    64
                                                                                        297 VPKDVDVILVAPKGSGRTVRTLFREGRGINSSIAVYQDVTGKAKEKAIAMGVAVGSGYLY
                                                                                                                                                                                                                                                                                                                                                                  STTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEATQSLYPLI
                                                                  QAARLICNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETVYERA
                                                                                                                                     DWPREKLLDYFKNDTFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWKAAIEDGWVP
                                                                                                                                                                                                                                                                            PPKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVAIGSGYVY
                                                                                                                                                                                                                                                                                                                                              QTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEATQSLYPLI
                                  Gaps
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DB 6; Length 500;
                                  60; Indels
70.6%; Score 1462.5; DB 6
71.6%; Pred. No. 6.7e-129;
ive 46; Mismatches 60;
              Local Similarity 71.6
nes 275; Conservative
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   Query Match
                   Best Loca
Matches
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416

357

19 KRTFALATRAAAYSRPAARFVKPMITT----RGLKQINFGGTVETVYERADWPREKLL

Gaps

6

57; Indels

Mismatches

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Conservative

275;

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Carbamoytransferase (OCTase) or ketol-acid reductoisomerase polypeptide,

or fungal pathogenicity-conferring gene with a test compound. The method

comprises: contacting OCTase polypeptide, ketol-acid reductoisomerase

polypeptide, or fungal pathogenicity-conferring gene with a test compound

; and detecting the presence or absence of binding between the test

compound and the polypeptide or gene, where binding between the test

test compound and the polypeptide or gene, where binding indicates that the

test compound at least 50% sequence encoding at least

10% of the activity of, 400, 403 or 469 amino acids; and an isolated

polypeptide consisting essentially of the amino acid sequence of 400, 403

or 469 amino acids. The methods are useful for identifying inhibitors of

ornithine carbamoytransferase, ketol-acid reductoisomerase, and fungal

pathogenicity-conferring gene as antibiotics. This is the amino acid

sequence of Mycosphaerella graminicola ketol-acid reductoisomerase KARI.
                                  364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a test compound as a candidate for an antibiotic comprises contexting ornithine carbamoytransferase (OCTase) or ketol-acid reductoisomerase polypeptide, or fungal pathogenicity-conferring gene with a test compound.
GKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFNSQPDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a method of identifying a test compound as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SA, Heiniger RW;
Shuster JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         graminicola ketol-acid reductoisomerase KAR1 segid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lo SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          substrate inhibition; antibiotic; gene disruption;
ketol-acid reductoisomerase; KAR1; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chamorro MV, Darveaux BA, Frank S
Pan H, Covington AS, Tarpey R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dezwaan TM,
                                                                                                                              REKLEKELDTIRNMEIWKVGKEVR 388
                                                                                                                                                                       Claim 50; SEQ ID NO 9; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADV16802, ADV16808, ADV16809.
                                                                                                                                                                                                                                                                                                                                                         ADV16810 standard; protein; 403 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adachi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PARA-) PARADIGM GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAY-2003; 2003US-0470947P.
19-MAY-2003; 2003US-0471615P.
21-MAY-2003; 2003US-0472242P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-2004; 2004WO-US015404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycosphaerella graminicola.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hamer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2005-021202/02
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Mahanty SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-DEC-2004
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305
                                                             417
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Score 1448.5; DB 9; Length 403; Pred. No. 1e-127;

69.9**%**; 72.0**%**;

Query Match Best Local Similarity

Sequence 403 AA;

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132
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                                                                                                                                                                          260
                                                  200
                                                                                                                                              252
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                                                                                                                                                                                                                  261 YSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEATQSLYPLIGKNGMDYM 320
                                                                                                                                                                                                                                                                         YDACSTTARRGALDWYPIFKNALKPVFQDLYBSTKNGTETKRSLEFNSQPDYREKLEKEL 372
        80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel purified or isolated Cryptococcus neoformans nucleic acid molecule comprising a sequence encoding a polypeptide comprising a sequence not given in the specification. A polymuclectide of the invention has fungicide activity, and may have use in gene therapy. The nucleic acid is useful for preparing a use in gene treating an infection caused by Cryptococcus neoformans. The present sequence represents a C. neoformans sequence of the invention. Note: The sequence data for this patent is not represented in
73 DYFKNDTFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWKAAIEDGWVPGKNLFTVE
                                                                                                                                              LVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVAIGSGYVYQTTFEREV
                                                                                                                                                           201 LVAPKGSGRTVRTLFKEGRGINSSIAIFQDVTGKAEEKAIALGVAVGSGYMYKTTFEKEV
                                                                                                                                                                                                    NSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEATQSLYPLIGKYGMDYM
                                                                                       133 DAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGKTLYFSHGFSPVFKDLTHVEPPKDLDVI
                                                                                                         New nucleic acid, useful for preparing a composition for treating an infection caused by Cryptococcus neoformans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C. neoformans amino acid sequence SEQ ID NO:3168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; SEQ ID NO 3168; 136pp; English.
                                                                                                                                                                                                                                                                                                                 394
                                                                                                                                                                                                                                                                                                                                ADB70124 standard; protein; 409 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fungicide; gene therapy; infection
                                                                                                                                                                                                                                                                                                                 DTIRNMEIWKVGKEVRKLRPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-DEC-2001; 2001US-0341261P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-DEC-2002; 2002WO-US040225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cryptococcus neoformans.
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121
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                                                                                                                                                                  WVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGKTLYFSHGFSPVFKDLT 181
                                                                                                                                                                                                                                                 YVYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEATQSLY 301
                                                                                                                                                                                                                                                                                       PLIGKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTKNGTETKRSLEFNSQ 361
                                                                                                                                                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening
                                                                                                          63
                                                                                        19
                                                                                                 ERADWPREKLLDYFKNDTFALIGYGSQGYGQGLNLRDNGLNVIIGVRKDGASWKAAIEDG
                                                                                                                                                                                                         HVEPPKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKAHEKAQALAVAIGSG
                                                                                     2 LRTQAARLICNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETVY
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Xu HH;
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                                                                   11;
                                                 409;
                                                Length
                                                                   64; Indels
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Forsyth |
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                                                DB 7;
                                              67.2%; Score 1392.5; DB 7;
68.5%; Pred. No. 2.1e-122;
iive 48; Mismatches 64;
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Yamamoto R
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072881.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                  267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prokaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteroides fragilis.
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Trawick JD,
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                                                         Local Similarity
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                            Sequence 409
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                                                Query Match
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Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                  Matches
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the invention fractate to an interest and understanding any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense conding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of agene in an operon required for proliferation or the activity of agene in an operon required for the gene product or that has an activity against a biological pathway required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the collection of an organism. The antisense nucleic acids are useful for for collectional description of an organism. The antisense nucleic acids are quired for collectional descriptions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 RKDGASWKAAIEDGWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTKGKTL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 AFNETVEELIGSLMPLFAKNGMDWMYANCSTTAQRGALDWMGPFHDAIKPVVQKLYNSVK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed the printed specification of the printed ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 AFNETVEEATOSLYPLIGKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFQDLYESTK 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 HEKAQALAVAIGSGYVYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 YFSHGFSPVFKDLTHVEPPKDLDVILVAPKGSGRTVRSLFKEGRGINSSYAVWNDVTGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs
                                                                                                                                      The invention relates to an isolated nucleic acid comprising any
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 53.1%; Score 1099.5; DB Best Local Similarity 59.4%; Pred. No. 8.2e-95, Matches 206; Conservative 53; Mismatches 87
                                                                             SEQ ID NO 48900; 1766pp; English.
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Job time : 115.517 secs
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                                                                               Claim 25;
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